

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2006, 06:54:58 ; Search time 5124 Seconds  
(without alignments)  
10317.020 Million cell updates/sec

Title: US-09-825-882-7

Perfect score: 930

Sequence: 1 atgataactttctaccat.....agaagacttcctccatag 930

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_av.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	930	100.0	930	6	BD144616 Novel G-p
2	930	100.0	930	8	AY114089 Homo sapi
3	930	100.0	1330	6	AX647299 Sequence
4	930	100.0	110000	14	AC018743 0
5	930	100.0	167868	8	AC018630 Homo sapi
6	925.2	99.5	930	8	AY724943 Homo sapi
7	924	99.4	930	6	CS008113 Sequence
8	923.2	99.3	930	8	AF494237 Homo sapi
9	922.2	99.2	927	6	CQ800006 Sequence
10	917.2	98.6	930	8	AY724889 Pan trogl
11	915.2	98.4	930	8	AY677147 Pan panis
12	865.6	93.1	930	8	AY724849 Pan panis
13	863.6	92.9	870	8	AY736059 Pan trogl
14	861.2	92.6	930	8	AY724878 Pan panis
15	859.2	92.4	930	8	AY677148 Pan panis
16	858	92.3	930	8	AY724974 Pongo pyg
17	857	92.2	857	8	AB199182 Homo sapi
18	853.2	91.7	930	8	AY724942 Homo sapi

19	852.8	91.7	930	6	CS008269 Sequence
20	851.6	91.6	930	6	BD144621 Novel G-p
21	851.6	91.6	930	8	AY114090 Homo sapi
22	851.6	91.6	1330	6	AX647301 Sequence
23	851.2	91.5	930	6	CS008275 Sequence
24	851.2	91.5	930	8	AF494228 Homo sapi
25	850.4	91.4	930	6	CS008115 Sequence
26	850.2	91.4	927	6	CQ800008 Sequence
27	849.6	91.4	930	6	CS008271 Sequence
28	849.6	91.4	930	6	CS008277 Sequence
29	848	91.2	930	6	CS008273 Sequence
30	848	91.2	930	6	CS008279 Sequence
31	848	91.2	930	6	CS008281 Sequence
32	844.2	90.8	857	8	AB199183 Pan trogl
33	840	90.3	930	8	AY724912 Gorilla g
34	835.6	89.8	930	8	AY724848 Pan panis
35	832.4	89.5	930	8	AY677150 Pan panis
36	830	89.2	930	8	AY724877 Pan trogl
37	829.2	89.2	930	6	CS008289 Sequence
38	829.2	89.2	930	8	AY114091 Homo sapi
39	829.2	89.2	1330	6	AX647391 Sequence
40	827.6	89.0	930	6	CS008287 Sequence
41	827.6	89.0	930	6	CS008291 Sequence
42	827.6	89.0	930	8	AY677149 Pan panis
43	827.2	88.9	930	8	AY724941 Homo sapi
44	826	88.8	930	6	CS008283 Sequence
45	825.6	88.8	888	8	AY736056 Pan trogl

## ALIGNMENTS

RESULT 1	BD144616	BD144616	Novel G-protein coupled receptors.	930 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	BD144616	BD144616	Novel G-protein coupled receptors.				
ACCESSION	BD144616	BD144616	Novel G-protein coupled receptors.				
VERSION	BD144616.1	GI:27850374					
KEYWORDS	JP 2002112793-A/341.						
SOURCE	Homo sapiens (human)						
ORIGIN	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;						
	Hominidae; Homo.						
REFERENCE	1 (bases 1 to 930)						
AUTHORS	Haga, T., Takeda, S. and Miyake, N.						
TITLE	Novel G-protein coupled receptors						
JOURNAL	Patent: JP 2002112793-A 341 16-APR-2002;						
	JAPAN SCIENCE AND TECHNOLOGY CORP						
COMMENT	OS Homo sapiens (human)						
	PN JP 2002112793-A/341						
	PD 16-APR-2002						
	PF 09-FEB-2001 JP 2001034434						
	PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE						
	PC						
	C12N15/09,A01K67/027,A61K38/00,A61K39/395,A61K45/00, PC						
	A61K48/00,						
	PC A61P43/00,C07K14/705,C07K19/00,C12N1/15,C12N1/19, PC						
	C12N1/21,						
	C12N5/10,C12Q1/02,C12Q1/68,G01N33/15,G01N33/53, PC						
	C12N3/566//						
	C12P21/08,C12N15/00,A61K37/02,C12N5/00						
	Novel G-protein coupled receptors						
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FEATURES	source						
ORIGIN							
Query Mat.	100.0%; Score 930; DB 6; Length 930;						

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		Matches	930;	Conservative	0;					
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Db	1	ATGATAAATCTTTCTACCCATCAATTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGA	60							
QY	61	AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGACACAAAG	120							
Db	61	AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGACACAAAG	120							
QY	121	ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGTTTGTCTGG	180							
Db	121	ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGTTTGTCTGG	180							
QY	181	GTATTATTAAATCGGTGATTAATCACTGTTGAATCCAGCTTTTAATAGTAGTAGAAGTA	240							
Db	181	GTATTATTAAATCGGTGATTAATCACTGTTGAATCCAGCTTTTAATAGTAGTAGAAGTA	240							
QY	241	AGAACTACTGCTTATAATATCTGGCGAGTGATCAACCAATTTTCAGCAACTGGCTTGTACT	300							
Db	241	AGAACTACTGCTTATAATATCTGGCGAGTGATCAACCAATTTTCAGCAACTGGCTTGTACT	300							
QY	301	ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCAC	360							
Db	301	ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCAC	360							
QY	361	TTAAAGAGGAGATTAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTG	420							
Db	361	TTAAAGAGGAGATTAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTG	420							
QY	421	GCTTGTCATCTTTTGTGATAAATCAATGATGATGTTGCGGACAAAGAAATTTGAAGA	480							
Db	421	GCTTGTCATCTTTTGTGATAAATCAATGATGATGTTGCGGACAAAGAAATTTGAAGA	480							
QY	481	AACATGACTTGAAGATCAAAATGAAGAGTGCAATGATCTTTTCAAATGATGCTGAACC	540							
Db	481	AACATGACTTGAAGATCAAAATGAAGAGTGCAATGATCTTTTCAAATGATGCTGAACC	540							
QY	541	ATGGTAGCAAACTTAGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT	600							
Db	541	ATGGTAGCAAACTTAGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT	600							
QY	601	TCCTTTGTAAACATCTCAAGAGATGCACTCCATGTTAAAGGATCTCAAGATCCCAGC	660							
Db	601	TCCTTTGTAAACATCTCAAGAGATGCACTCCATGTTAAAGGATCTCAAGATCCCAGC	660							
QY	661	ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTTGTGTTATGTCGCAAT	720							
Db	661	ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTTGTGTTATGTCGCAAT	720							
QY	721	TACTTTCTGTCATAATGATATCAGTTTGGAGTTTGGAACTCTGGAAACAAACCTGTC	780							
Db	721	TACTTTCTGTCATAATGATATCAGTTTGGAGTTTGGAACTCTGGAAACAAACCTGTC	780							
QY	781	TTTCATGTTCTGCAAGCTATTAGATTCAGTATCTTCAATCCACCTTCACTCTGATT	840							
Db	781	TTTCATGTTCTGCAAGCTATTAGATTCAGTATCTTCAATCCACCTTCACTCTGATT	840							
QY	841	TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTTTTCAGTTTGTGGCAATGAGGTACTGG	900							
Db	841	TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTTTTCAGTTTGTGGCAATGAGGTACTGG	900							
QY	901	GTGAAGGAGAGAGACTTCTATCTCCATAG	930							
Db	901	GTGAAGGAGAGAGACTTCTATCTCCATAG	930							

RESULT 2  
AY114089  
LOCUS  
DEFINITION  
ACCESSION

AY114089  
Homo sapiens putative taste receptor T2R52 gene, complete cds.  
AY114089  
linear  
PRI 28-FEB-2003

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Y114089.1 GI:28603627

Homo sapiens (human)

ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Cimidae; Homo.  
(bases 1 to 930)  
Identification and characterization of human taste receptor genes  
belonging to the TAS2R family  
Cytogenet. Genome Res. 98 (1), 45-53 (2002)

12584440

2 (bases 1 to 930)

Conte, C., Ebelin, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.

Direct Submission  
Submitted (17-MAY-2002) Pharma Research Basel, F. Hoffmann-La Roche  
Ltd., Grenzachstrasse 124, Basel CH-4070, Switzerland

Location/Qualifiers

FEATURES

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ORIGIN

Query Match

Best Local Similarity 100.0%; Score 930; DB 8; Length 930;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGATAAATCTTTCTACCCATCAATTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGA 60

QY 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGACACAAAG 120

Db 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGACACAAAG 120

QY 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGTTTGTCTGG 180

Db 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGTTTGTCTGG 180

QY 181 GTATTATTAAATCGGTGATTAATCACTGTTGAATCCAGCTTTTAATAGTAGTAGAAGTA 240

Db 181 GTATTATTAAATCGGTGATTAATCACTGTTGAATCCAGCTTTTAATAGTAGTAGAAGTA 240

QY 241 AGAACTACTGCTTATAATATCTGGCGAGTGATCAACCAATTTTCAGCAACTGGCTTGTACT 300

Db 241 AGAACTACTGCTTATAATATCTGGCGAGTGATCAACCAATTTTCAGCAACTGGCTTGTACT 300

QY 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCAC 360

Db 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCAC 360

QY 361 TTAAAGAGGAGATTAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTG 420

Db 361 TTAAAGAGGAGATTAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTG 420

QY 421 GCTTGTCATCTTTTGTGATAAATCAATGATGATGTTGCGGACAAAGAAATTTGAAGA 480

Db 421 GCTTGTCATCTTTTGTGATAAATCAATGATGATGTTGCGGACAAAGAAATTTGAAGA 480

Db 421 GCTTGTCTATCTTTTGTGATTAACATGATGAGATTGTGCGGACAAAGAAATTTGAAGA 480  
Qy 481 AACATGACTTGAAGATCAAAATTTGAAGATGCAATGTACTTTTCAAATATGACTGTAAAC 540  
Db 481 AACATGACTTGAAGATCAAAATTTGAAGATGCAATGTACTTTTCAAATATGACTGTAAAC 540  
Qy 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCTACTACTTTTATGCTGTATCTGT 600  
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Qy 601 TCTTTTGTAAACATCTCAAGAGATGAGCTTCCATGTTAAAGGATCTCAAGATCCCAGC 660  
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Qy 661 ACCAAGGTCCACATAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCAAT 720  
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Qy 721 TACTTTCTGTCATATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
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Qy 781 TTATGTTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCTCTGATT 840  
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Qy 841 TGGGAAACAAAGACTTAAAGCAGACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
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Qy 901 GTGAAGGAGAGAGACTTCTATCTCCATAG 930  
Db 901 GTGAAGGAGAGAGACTTCTATCTCCATAG 930

## RESULT 3

AX647299 AX647299 1330 bp DNA linear PAT 04-MAR-2003  
LOCUS Sequence 1491 from Patent EP1270724.  
DEFINITION AX647299  
ACCESSION AX647299  
VERSION AX647299.1 GI:28800813  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1

REFERENCE Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.  
AUTHORS Guanosine triphosphate-binding protein coupled receptors  
TITLE Patent: EP 1270724-A 1491 02-JAN-2003;  
JOURNAL National Institute of Advanced Industrial Science and Technology  
(JP); Center for Advanced Science and Technology Incubation, Ltd.  
(JP)

## FEATURES

## source

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## ORIGIN

Query Match 100.0%; Score 930; DB 6; Length 1330;  
Sequence split into 5 fragments LOCUS AC018743 Accession AC018743  
Fragment Name Begin End

Best Local Similarity 100.0%; Pred. No. 4.6e-181;  
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 261 AATTTTGTAAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAAG 320  
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Qy 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTCAGCAACCTGGCTTGTACT 300  
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Qy 361 TTAAAGAGGAGATTAAGAGTGTCTATCTGTTGATGTTGTTGGGCGCTTTGCTATTATTG 420  
Db 561 TTAAAGAGGAGATTAAGAGTGTCTATCTGTTGATGTTGTTGGGCGCTTTGCTATTATTG 620  
Qy 421 GCTTGTCTATCTTTTGTGATAAACAATGAGATTGTGCGGACAAAAGAAATTTGAAGGA 480  
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Qy 481 AACATGACTTGGAGATCAAAATTTGAGAGTGCATGTACTTTTCAAATATGACTGTAAAC 540  
Db 681 AACATGACTTGGAGATCAAAATTTGAGAGTGCATGTACTTTTCAAATATGACTGTAAAC 740  
Qy 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGT 600  
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Qy 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCAATCTCTGATT 840  
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Qy 841 TGGGAAACAAAGAGCTTAAAGCAGACTTTTCTTCTGAGTTTTTGGCAATGAGGTACTGG 900  
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## RESULT 4

AC018743 0/c

## WPCOMMENT

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AC018743\_2 200001 310000  
AC018743\_3 300001 410000  
AC018743\_4 400001 466818

LOCUS AC018743 466818 bp DNA linear HTG 17-JUN-2003  
DEFINITION Homo sapiens chromosome 12 clone RP11-289M22, WORKING DRAFT  
ACCESSION AC018743  
VERSION AC018743.27 GI:31791062  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

1 (bases 1 to 466818)  
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,  
Albrooks, S.L., Amaratunge, H.C., Are, J.R., Ayelle, M., Banks, T.,  
Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,  
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,  
Buahy, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,  
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,  
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,  
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,  
Davilla, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,  
Delaney, K.K., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,  
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,  
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,  
Falle, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,  
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,  
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Harris, C., Harris, K., Hart, M., Haviak, P., Hawes, A., Hernandez, J.,  
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Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,  
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,  
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,  
Kratovic, J., Kurashi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,  
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,  
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louissegh, H.,  
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Massey, E., Mahoney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,  
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,  
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,  
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,  
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Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
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Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 466818)  
Worley, K.C.

Direct Submission  
Submitted (18-DEC-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 466818)  
Worley, K.C.

Direct Submission  
Submitted (17-JUN-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jun 17, 2003 this sequence version replaced gi:21431021.  
----- Genome Center

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Drafting Center Code: BCM  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HMDC  
Center clone name: RP11-289M22  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 463747 bases at least Q40  
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Quality coverage: 4x in Q20 bases; sum-of-contrigs estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 30 contrigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contrigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ATCTCTTTGTGACAAATCTCACTGCTGCGGGTCTCCAGAGTTGTTTGTCTGG 180

Db 21188 ATCTCTTTGTGACAAATCTCACTGCTGCGGGTCTCCAGAGTTGTTTGTCTGG 21129

QY 181 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTTAGAAGTA 240

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## RESULT 5

AC018630

LOCUS

DEFINITION

AC018630

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

1 (bases 1 to 167868)

REFERENCE

AUTHORS

1 (bases 1 to 167868)

Muzny,D.M., Adams,C., Ali-Osman,B., Ali-Osman,F.R., Allen,C.,

Albrooks,S.L., Amaral, J., Bimonte,N., Bimonte,N., Bimonte,N.,

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Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Haves, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollings, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Joshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Liu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheehwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Mettaker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Oguh, M., Okwuonu, G., Oreguine, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, J.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoohtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstein, G. and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 167869)  
Worley, K.C.  
Direct Submission  
Submitted (15-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 167869)  
Worley, K.C.  
Direct Submission  
Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
4 (bases 1 to 167869)  
Worley, K.C.  
Direct Submission  
Submitted (30-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
5 (bases 1 to 167869)  
Worley, K.C.  
Direct Submission  
Submitted (24-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
6 (bases 1 to 167869)  
Worley, K.C.  
Direct Submission  
Submitted (15-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Aug 30, 2002 this sequence version replaced gi:22450371.  
Information: <http://www.hgsc.bcm.tmc.edu/> or email [gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:  
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.  
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.  
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.  
SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.  
QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.  
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ACCESSION        CS008113
VERSION          CS008113.1  GI:59669019
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REFERENCE         1
AUTHORS          Drayna,D. and Kim,U.K.
TITLE            Variants of human taste receptor genes
JOURNAL          Patent: WO 2005007891-A 31 27-JAN-2005;
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DEFINITION AF494237
ACCESSION AF494237.1 GI:20336530
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 930)
AUTHORS Bufo, B., Hofmann, T., Krautwurst, D., Ragnuse, J.-D. and Meyerhof, W.
TITLE The human TAS2R16 receptor mediates bitter taste in response to
beta-glucopyranosides
JOURNAL Nat. Genet. 32 (3), 397-401 (2002)
PUBMED 12379855
REFERENCE 2 (bases 1 to 930)
AUTHORS Bufo, B., Hofmann, T., Krautwurst, D., Ragnuse, J.-D. and Meyerhof, W.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2002) Molecular Genetics, German Institute of
Human Nutrition, Arthur-Scheunert Allee 114-116, Potsdam-Rehbrücke
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VERSION CQ800006.1 GI:46848948
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Hominoidea; Homo.
REFERENCE 1
AUTHORS Bufo, B., Hofmann, T., Krautwurst, D., Kuhn, C. and Meyerhof, W.
TITLE Bitter taste receptors
JOURNAL Patent: WO 2004029087-A 10 08-APR-2004;
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ACCESSION	AY724889					
VERSION	AY724889.1	GI:51989096				
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SOURCE	Pan troglodytes					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Pan.					
REFERENCE	1 (bases 1 to 930)					
AUTHORS	Fischer,A., Gilad,Y., Mar,O. and Paabo,S.					
TITLE	Evolution of Bitter Taste Receptors in Humans and Apes					
JOURNAL	Mol. Biol. Evol. 22 (3), 432-436 (2005)					
PUBMED	15496549					
REFERENCE	2 (bases 1 to 930)					
AUTHORS	Anne,F., Yoav,G., Orna,N. and Svante,P.					
TITLE	Direct Submission					
JOURNAL	Submitted (12-AUG-2004) Genetics, Max-Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany					
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Qy	61	AATTTTGTAAATGGCTTCATAGCAGTGGTAAATCCATTGAGTGGTTCAAGAGACAAAAG	120			
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DEFINITION
ACCESSION AY677147
VERSION AY677147.1 GI:54111484
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominoidea; Pan.
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1 (bases 1 to 930)
PARTY,C.M., Erkner,A. and le Coutre,J.
Divergence of T2R chemosensory receptor families in humans,
bonobos, and chimpanzees
Proc. Natl. Acad. Sci. U.S.A. 101, 14830-14834 (2004)
15466715
JOURNAL
PUBMED
2 (bases 1 to 930)
PARTY,C.M., Erkner,A. and le Coutre,J.
Direct Submission
AUTHORS
TITLE
Submitted (05-JUL-2004) Nestle Research Centre, P.O. Box 44,
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 1 (bases 1 to 930)  
 Fischer, A., Glad, Y., Man, O. and Paabo, S.  
 Evolution of Bitter Taste Receptors in Humans and Apes  
 Mol. Biol. Evol. 22 (3), 432-436 (2005)  
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 2 (bases 1 to 930)  
 Anne, F., Yoav, G., Orna, M. and Svante, P.  
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 1 (bases 1 to 870)  
 Wang, X., Thomas, S.D. and Zhang, J.  
 Relaxation of selective constraint and loss of function in the  
 evolution of human bitter taste receptor genes  
 Hum. Mol. Genet. 13 (21), 2671-2678 (2004)  
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 PUBMED  
 REFERENCE  
 2 (bases 1 to 870)  
 Zhang, J., Wang, X. and Thomas, S.D.  
 Direct Submission  
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Fischer,A., Gilad,Y., Man,O. and Paabo,S.			
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Anne,F., Yoav,G., Orna,M. and Svante,P.			
AUTHORS			
Direct Submission			
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DEFINITION Pan paniscus  
ACCESSION AY677148  
VERSION  
KEYWORDS  
SOURCE Pan paniscus (pygmy chimpanzee)  
ORGANISM Pan paniscus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Pan.  
1 (bases 1 to 930)  
REFERENCE  
AUTHORS Parry,C.M., Erkner,A. and le Coutre,J.  
TITLE Divergence of T2R chemosensory receptor families in humans,  
bonobos, and chimpanzees  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101, 14830-14834 (2004)

15466715  
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Parry,C.M., Erkner,A. and le Coutre,J.  
Direct Submission  
JOURNAL Submitted (05-JUL-2004) Nestle Research Centre, P.O. Box 44,  
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GenCore version 5.1.7  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	930	100.0	930	13	ADR29239
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9	922.2	99.2	927	13	ADM33296
10	852.8	91.7	930	14	ADM74575
11	851.6	91.6	930	6	AAS18169
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14	851.6	91.6	930	13	ADR29243
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23	848	91.2	930	14	ADM74585	Adw74585 Human bit
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25	829.2	89.2	930	6	AAS18173	Aas18173 Human T2R
26	829.2	89.2	930	8	ACC44475	Acc44475 Gene enco
27	829.2	89.2	930	13	ADR29251	Adr29251 Taste rec
28	829.2	89.2	930	14	ADM74595	Adw74595 Human bit
29	829.2	89.2	1330	10	ADC87130	Adc87130 Human GPC
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ALIGNMENTS

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AC AAS18167;  
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DT 26-MAR-2002 (first entry)  
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XX  
KW Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor;  
KW ht2R61; T2R61; T2R; bitter taste sensation; taste signalling pathway; ss;  
KW taste transduction; food taste masking; drug taste masking.  
XX  
OS Homo sapiens.  
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FH Key Location/Qualifiers  
CDS 1..930  
FT /\*tag= a  
FT /product= "Human T2R61"  
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PN WO200177676-A1.  
XX  
PD 18-OCT-2001.  
XX  
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PR 07-APR-2000; 2000US-0195532P.  
PR 13-NOV-2000; 2000US-0247014P.  
XX  
(SENO-) SENOMYX INC.  
PI Adler JE;  
XX  
DR WPI; 2002-017486/02.  
DR P-PSDB; AAU11384.  
XX  
Novel isolated mammalian taste cell-specific G protein-coupled receptor,  
T2R, involved in bitter taste sensation, useful for identifying taste  
modulators that are used to decrease or mask bitter taste of foods or  
drugs.  
XX

```
PS Claim 1; Page 72; 103pp; English.
XX
CC The invention relates to a mammalian taste cell-specific G protein-
CC coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste
CC sensation. The T2R polypeptides and their associated polynucleotides are
CC useful for screening one or more compounds for the presence of taste
CC detectable by a mammal. Modulators of T2R polypeptides (modulators of
CC taste transduction) are useful for pharmacological and genetic
CC modulations of taste signalling pathways. These modulatory compounds are
CC then used in food and pharmaceutical industries to customise taste, e.g.,
CC to decrease or mask the bitter taste of foods or drugs. This sequence
CC represents cDNA encoding the human T2R61 (hr2R61) polypeptide
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Best Local Similarity 100.0%; Pred. No. 1.2e-247;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200216548-A2.
XX
PD 28-FEB-2002.
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PF 30-JUL-2001; 2001WO-1B001446.
XX
PR 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Haga T, Takeda S, Mitaku S;
XX
DR WPI; 2002-304118/34.
XX
P-PSDB; ABP95936.
PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
PS Claim 9; SEQ ID NO 681; 97pp + Sequence Listing; Japanese.
XX
CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95936-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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## RESULT 3

ABZ68712

ID ABZ68712 standard; DNA; 930 BP.

XX AC

XX ABZ68712;

XX DT

XX 16-MAY-2003 (first entry)

XX DE

XX Nucleotide sequence of human T2R61 polypeptide.

XX KW

XX Human; T2R4; G protein coupled receptor; GPCR; taste receptor;

XX KW

XX bitter alkaloid quinine; denatonium; 6-nitrosaccharin; T2R44; T2R61;

XX KW

XX bitter taste; saccharin; Gene; ss.

XX XX

OS Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS

XX 1..930

XX /\*tag= a

XX /product= "T2R61"

XX

XX WO2003006482-A2.

XX

XX 23-JAN-2003.

XX

XX 10-JUL-2002; 2002WO-US021602.

XX

XX 10-JUL-2001; 2001US-0303811P.

XX

XX 15-APR-2002; 2002US-0372089P.

XX

XX (SENO-) SENOMYX INC.

XX

XX Pronin A, Connor J, Tang H, Keung W, Servant G, Adler JB;

XX PI

XX O'Connell S, Brust P;

XX

XX WPI; 2003-221711/21.

XX

XX P-PSDB; ABP97669.

XX

XX Assay method for identifying a compound, which modulates hT2R4 associated

XX bitter taste, involves screening a compound for its effect on quinine or

XX a structurally related compound to induce activation of hT2R4.

XX

XX PS

XX Disclosure; Page 11-12; 82pp; English.

XX

XX The present sequence encodes a human T2R61 protein. T2R61 is a G protein

XX coupled receptor (GPCR) that is specifically activated by the bitter

XX derivative of saccharin, 6-nitrosaccharin. T244 is activated by

XX denatonium and 6-nitrosaccharin. T2R4 is activated by the bitter alkaloid

XX quinine. The specification describes an assay for identifying compounds

XX which modulate T2R4, T2R61 and T2R44 associated bitter taste. The

XX identified compounds are used in foods, beverages and medicines to

XX inhibit bitter taste e.g. saccharin containing diet beverages, foods or

XX medicinal products

XX

XX SQ

XX Sequence 930 BP; 255 A; 177 C; 179 G; 319 T; 0 U; 0 Other;

XX

XX Query Match

XX 100.0%; Score 930; DB 8; Length 930;

XX Best Local Similarity

XX 100.0%; Pred. No. 1.2e-247;

XX Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX Qy

XX 1 ATGATAACTTTTTCACCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

XX Db

XX 1 ATGATAACTTTTTCACCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

XX

XX Qy

XX 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTTCCATTGAGTGGTTCAAGAGACAAAAG 120

XX Db

XX 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTTCCATTGAGTGGTTCAAGAGACAAAAG 120

XX

XX Qy

XX 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG 180

XX Db

XX 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG 180

XX

XX Qy

XX 181 GTATTATTATTAACCTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240

XX Db

XX 181 GTATTATTATTAACCTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240

XX

XX Qy

XX 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTGTCTACT 300

XX Db

XX 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTGTCTACT 300

XX

XX Qy

XX 301 ACCCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCCAACCTTTATTTTCTTCCAC 360

XX Db

XX 301 ACCCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCCAACCTTTATTTTCTTCCAC 360

XX

XX Qy

XX 361 TTAAGAGAGAGATTAAAGAGTGTCAATCTGGTGAATGTTGTTGGGCTTTGTCTATTTTGG 420

XX Db

XX 361 TTAAGAGAGAGATTAAAGAGTGTCAATCTGGTGAATGTTGTTGGGCTTTGTCTATTTTGG 420

```
QY 421 GCTTGTCTCTTTTGTGATAAACAATGATGAGATTGTGCGACAAAAGAAATTTGAAGA 480
DB 421 GCTTGTCTCTTTTGTGATAAACAATGATGAGATTGTGCGACAAAAGAAATTTGAAGA 480
QY 481 AACATGACTTGGAGATCAAAATGGAAGTGCATGTACTTTTCAAAATGACTCTAACC 540
DB 481 AACATGACTTGGAGATCAAAATGGAAGTGCATGTACTTTTCAAAATGACTCTAACC 540
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTATGCTGTTAATCTGT 600
DB 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTATGCTGTTAATCTGT 600
QY 601 TCTTTGTGTAAACATCTCAAGAGATGCGAGCTCCATGGTAAAGGATCTCAAGATCCCAGC 660
DB 601 TCTTTGTGTAAACATCTCAAGAGATGCGAGCTCCATGGTAAAGGATCTCAAGATCCCAGC 660
QY 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCAATT 720
DB 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCAATT 720
QY 721 TACTTTCTGTCATTAATGATATCAGTTTGGAGTTTGGAAAGTCTGGAAGAAACAAACCTGTC 780
DB 721 TACTTTCTGTCATTAATGATATCAGTTTGGAGTTTGGAAAGTCTGGAAGAAACAAACCTGTC 780
QY 781 TTCATGTTCTGCAAGCTATTAGATTCAGTATCTCCTTCAATCCACCCATTCACTCTGATT 840
DB 781 TTCATGTTCTGCAAGCTATTAGATTCAGTATCTCCTTCAATCCACCCATTCACTCTGATT 840
QY 841 TGGGAAACAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGGAAATGAGTACTGG 900
DB 841 TGGGAAACAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGGAAATGAGTACTGG 900
QY 901 GTGAAGAGGAGAGAACTTCACTCTCCATAG 930
DB 901 GTGAAGAGGAGAGAACTTCACTCTCCATAG 930
```

## RESULT 4

AD132659

ID AD132659 standard; DNA; 930 BP.

XX

AC AD132659;

XX

DT 22-APR-2004 (first entry)

XX

DE Human taste receptor-related THTR9 DNA.

XX

KW G protein-coupled receptor; GPCR; food processing; seasoning; human;

XX

KW taste receptor; THTR9; db.

XX

OS Homo sapiens.

XX

PN WO2004007716-A1.

XX

PD 22-JAN-2004.

XX

PF 17-JUL-2003; 2003WO-JP009093.

XX

PR 17-JUL-2002; 2002JP-00208284.

XX

PA (UYN1-) UNIV NIPPON.

XX

PI Takao K, Suga H, Takao T;

XX

DR WPI; 2004-122947/12.

XX

PT Isolation of GPCR (G protein-coupled receptor) gene from human brain  
PT tissue for constructing vector and transformant to produce THTR taste  
PT receptor protein and screening its ligands for use in foods.

XX

PS Claim 9; SEQ ID NO 1; 84pp; Japanese.

XX

XX

CC The invention relates to a novel method for isolating a G protein-coupled  
CC receptor (GPCR) gene comprising designing primers based on sequence data  
CC for known GPCR genes and their surrounding domains, amplification with  
CC the use of these primers and cDNA libraries from tissues other than those  
CC expressing such genes, cloning the thus amplified fragment and  
CC identifying the cloned gene. The GPCR gene of the invention and its  
CC encoded protein may be applicable in screening for ligands that regulate  
CC taste which may then be used in food compositions e.g. for seasoning and  
CC food processing, as well as for providing a database for studying other  
CC genes. The current sequence is that of the human taste receptor-related  
CC THTR9 DNA of the invention.

XX

SQ Sequence 930 BP; 255 A; 177 C; 179 G; 319 T; 0 U; 0 Other;

## Query Match

100.0%; Score 930; DB 12; Length 930;

Best Local Similarity 100.0%; Pred. No. 1.2e-247;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTACCCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

DB 1 ATGATAACTTTTACCCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

QY 61 AATTTTGTAAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGAGACAAAAG 120

DB 61 AATTTTGTAAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGAGACAAAAG 120

QY 121 ATCTCCTTTGTCGACCAAAATTCACCTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180

DB 121 ATCTCCTTTGTCGACCAAAATTCACCTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180

QY 181 GTATTATTATTAAACTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240

DB 181 GTATTATTATTAAACTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240

QY 241 AGAATCTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAAGCACTGGCTTCTACT 300

DB 241 AGAATCTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAAGCACTGGCTTCTACT 300

QY 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCAACTTTTATTTTCTTCTCAC 360

DB 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCAACTTTTATTTTCTTCTCAC 360

QY 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTGTGTTGTTGGGGCTTTTGTATTTTGG 420

DB 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTGTGTTGTTGGGGCTTTTGTATTTTGG 420

QY 421 GCTTGTCTATCTTTTGTGATAAACATGAATGAGATGTGCGGACAAAAGAAATTTGAAGA 480

DB 421 GCTTGTCTATCTTTTGTGATAAACATGAATGAGATGTGCGGACAAAAGAAATTTGAAGA 480

QY 481 AACATGACTTGGAGATCAAAATGGAAGTGCATGTACTTTTCAAAATGACTCTAACC 540

DB 481 AACATGACTTGGAGATCAAAATGGAAGTGCATGTACTTTTCAAAATGACTCTAACC 540

QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTATGCTGTTAATCTGT 600

DB 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTATGCTGTTAATCTGT 600

QY 601 TCTTTGTGTAAACATCTCAAGAGATGCGAGTCCATGGTAAAGGATCTCAAGATCCCAGC 660

DB 601 TCTTTGTGTAAACATCTCAAGAGATGCGAGTCCATGGTAAAGGATCTCAAGATCCCAGC 660

QY 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCAATT 720

DB 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCAATT 720

QY 721 TACTTTCTGTCATTAATGATATCAGTTTGGAGTTTGGAAAGTCTGGAAGAAACAAACCTGTC 780

DB 721 TACTTTCTGTCATTAATGATATCAGTTTGGAGTTTGGAAAGTCTGGAAGAAACAAACCTGTC 780

QY 781 TTCATGTTCTGCAAGCTATTAGATTCAGTATCTCCTTCAATCCACCCATTCACTCTGATT 840

DB 781 TTCATGTTCTGCAAGCTATTAGATTCAGTATCTCCTTCAATCCACCCATTCACTCTGATT 840

[illegible]

RESULT 5  
ADR29239  
ID ADR29239 standard; DNA; 930 BP.

04-NOV-2004' (first entry)

DE  
XX  
KW  
KW  
KW  
KW

Taste receptor modulation-related human T2R61 gene sequence SeqID178.

T1R; T2R; taste receptor; G protein; modulatory compound; MAPK activity; cAMP accumulation; adenylyl cyclase; bitter; taste; umami, sweet; T2R61; gene; ds; human.

Identifying a compound that modulates the activity of a T1R or T2R taste receptor by assaying the effect of the putative modulatory compound on MAPK activation, cAMP accumulation or adenylyl cyclase activity in the eukaryotic cell.

This invention is related to a novel method of identifying a compound that modulates the activity of a T1R or T2R taste receptor. The method comprises providing a eukaryotic cell that expresses a functional T1R or T2R taste receptor and a G protein that couples to it, contacting the eukaryotic cell with a compound and identifying whether the compound modulates the activity of T1R or T2R expressed by the eukaryotic cell based on its effect on MAPK activity, cAMP accumulation or adenylyl cyclase activity. The method is used to identify a compound or adenylyl bitter taste associated with a particular T2R activator or that blocks or enhances umami taste elicited by a compound that activates the T1R1/T1R3 (umami) taste receptor or sweet taste elicited by a compound that activates the T1R2/T1R3 (sweet) taste receptor. The method is useful in identifying a compound that modulates the activity of a T1R or T2R taste receptor. The present sequence is that of a gene which encodes a human T2R taste receptor and which is related to the method of the invention.

Query Match	100.0%	Score 930;	DB 13;	Length 930;
Best Local Similarity	100.0%	Pred. No. 1.2e-247;		
Matches 930;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ATGATAACCTTTCTACCCCATCATTTTCCAGTCTGGTAGTGGTTACATTGTTATTGGA 60

1	ATGATTAACATTTTCTACCAATCATTTTTTCCAGTCGTGGTAGTGGTTACATTTCTGTTATGGA	60
61	AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTAGTGTGTTCAAGAGACAAAG	120
61	AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTAGTGTGTTCAAGAGACAAAG	120
121	ATCTCTTTTGTGTGACCAAAATTTCTCACTGCTCTGGGGGTCTCAGAGTTGGTTTGTCTGG	180
121	ATCTCTTTTGTGTGACCAAAATTTCTCACTGCTCTGGGGGTCTCAGAGTTGGTTTGTCTGG	180
181	GTATTTATTATTAACCTGCTATTTCAACTGCTGTTTGAATCAGACTTTTAAATAGTGTAGAAGTA	240
181	GTATTTATTATTAACCTGCTATTTCAACTGCTGTTTGAATCAGACTTTTAAATAGTGTAGAAGTA	240
241	AGAACTACTGCTTATTAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTGTCTACT	300
241	AGAACTACTGCTTATTAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTGTCTACT	300
301	ACCCCTCAGCATATTTTATTTTGTCTCAAGATTGCGCAATTTCTCAACTTTATTTTTTCTTCAC	360
301	ACCCCTCAGCATATTTTATTTTGTCTCAAGATTGCGCAATTTCTCAACTTTATTTTTTCTTCAC	360
361	TTAAAGAGGAGAGTTTAAGAGTGTCAATCTCTGTTGATGTTGTTGGGGCCCTTGTCTATTTTGG	420
361	TTAAAGAGGAGAGTTTAAGAGTGTCAATCTCTGTTGATGTTGTTGGGGCCCTTGTCTATTTTGG	420
421	GCTTTGTCTATCTTTTTTGTGATAAACAATGAATCAGATTGTGCGGACAAAAGAAATTTGAAGA	480
421	GCTTTGTCTATCTTTTTTGTGATAAACAATGAATCAGATTGTGCGGACAAAAGAAATTTGAAGA	480
481	AACATGACTTTGGAAGATCAAAATTTGAAGTGCATGTAATTTTCAAAATATGACTGTAAACC	540
481	AACATGACTTTGGAAGATCAAAATTTGAAGTGCATGTAATTTTCAAAATATGACTGTAAACC	540
541	ATGCTAGCAAACTTAGTACCCCTTCACCTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT	600
541	ATGCTAGCAAACTTAGTACCCCTTCACCTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT	600
601	TCCTTTGTGTAACATCTCAAGAAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCACGC	660
601	TCCTTTGTGTAACATCTCAAGAAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCACGC	660
661	ACCAAGGTCCACATAAAAGCTTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCCATT	720
661	ACCAAGGTCCACATAAAAGCTTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCCATT	720
721	TACTTTCTGTCCATAATGATATACGTTTGGAGTTTGGAGTCTGGAAGTCTGGAAGCAAACTGTG	780
721	TACTTTCTGTCCATAATGATATACGTTTGGAGTTTGGAGTCTGGAAGTCTGGAAGCAAACTGTG	780
781	TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCTCTCAATCCACCCATTCATCTGATT	840
781	TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCTCTCAATCCACCCATTCATCTGATT	840
841	TGGGGAAACAAAGACTTAAAGCAGACTTTTCTTTTGTGCAAAATGAGGTACTGG	900
841	TGGGGAAACAAAGACTTAAAGCAGACTTTTCTTTTGTGCAAAATGAGGTACTGG	900
901	GTGAAAGGAGAGAGACTTTCATCTCCATAG	930
901	GTGAAAGGAGAGAGACTTTCATCTCCATAG	930
RESULT 6		
ACC44478		
ID	ACC44478 standard; DNA; 1179 BP.	
XX	ACC44478;	
XX	(first entry)	
DT	25-JUL-2003	
XX	Gene encoding human GI endocrine cell specific GPCR GT2R-h57.	
XX		

KW Chemosensor; G-protein coupled receptor; gene; ds; GPCR; receptor;  
KW gastrointestinal tract; taste; ion channel; endocrine cell.  
XX  
OS Homo sapiens.  
XX  
XX WO2003031604-A1.  
XX  
XX PD 17-APR-2003.  
XX  
XX PF 11-OCT-2002; 2002WO-US032664.  
XX  
XX PR 12-OCT-2001; 2001US-0328993P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA (PHLE/) PHLEGER C S W.  
XX  
XX Walsh JH, Rozengurt JE, Wu SV;  
XX  
XX WPI: 2003-381713/36.  
DR P-PSDB; ABR58042.  
XX  
XX New nucleic acid encoding a chemosensing G-protein coupled receptor,  
PT useful for identifying chemical sensing receptors and signaling molecules  
PT that allow pharmacological and genetic modulation of taste transduction  
PT pathways.  
XX  
XX Claim; Page 96; 101pp; English.  
XX  
XX This sequence represents a gene encoding a novel isolated chemosensing G-  
CC protein coupled receptor (GPCR) from the gastrointestinal tract. The  
CC nucleic acid is useful for identifying or isolating chemical sensing  
CC receptors (including taste ion channels) and signaling molecules that  
CC would allow pharmacological and genetic modulation of taste transduction  
CC pathways. The native STC-1 enteroendocrine cells that naturally express  
CC GR2R are useful in identifying modulators of taste receptor-mediated  
CC signal transduction. These cells are also used as models for studying  
CC taste-mediated signal transduction  
XX  
SQ Sequence 1179 BP; 314 A; 251 C; 226 G; 388 T; 0 U; 0 Other;

Query Match 100.0%; Score 930; DB 8; Length 1179;  
Best Local Similarity 100.0%; Pred. No. 1.3e-247;  
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTAACCTTTCTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60  
DB 250 ATGATAAATTTTCTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 309  
QY 61 AATTTTGTCTAATGGCTTCATAGCAGTGGTAAATTCATTGAGTGGTTCAGAGACAAAAG 120  
DB 310 AATTTTGTCTAATGGCTTCATAGCAGTGGTAAATTCATTGAGTGGTTCAGAGACAAAAG 369  
QY 121 ATCTCCTTTTGTGACCAAAATTCCTACTGCTCTGGGGGCTCCAGAGTTGGTTTGTCTGG 180  
DB 370 ATCTCCTTTTGTGACCAAAATTCCTACTGCTCTGGGGGCTCCAGAGTTGGTTTGTCTGG 429  
QY 181 GTATTATTATTAACCTGTAATTCAGTCTGGTGAATCCAGCTTTTAATAGTGTAGAGTA 240  
DB 430 GTATTATTATTAACCTGTAATTCAGTCTGGTGAATCCAGCTTTTAATAGTGTAGAGTA 489  
QY 241 AGAAGTACTGCTTATAATATCTGGGAGTGAATCAACCTTTTCAGCAACTGGCTTGTCTACT 300  
DB 490 AGAAGTACTGCTTATAATATCTGGGAGTGAATCAACCTTTTCAGCAACTGGCTTGTCTACT 549  
QY 301 ACCCTCAGCATATTTTATTGTTCTCAAGATGCGAATTTCTCAACTTTTATTATTCTTCTAC 360  
DB 550 ACCCTCAGCATATTTTATTGTTCTCAAGATGCGAATTTCTCAACTTTTATTATTCTTCTAC 609  
QY 361 TTAAGAGGAGAGTAAAGAGTGTCAATTCGGTGTAGTCTGTTGGGCTTTGCTATTATTG 420  
DB 610 TTAAGAGGAGAGTAAAGAGTGTCAATTCGGTGTAGTCTGTTGGGCTTTGCTATTATTG 669  
QY 421 GCTTGTGCATCTTTTGTGATAAATCATGAATGAGATTGTGCGGACAAAAGAAATTTGAAGGA 480

DB 670 GCTTGTGCATCTTTTGTGATAAATCATGAATGAGATTGTGCGGACAAAAGAAATTTGAAGGA 729  
QY 481 AACATGACTTGGAAAGATCAAAATTTGAAGAGTGCATGTAATTTTCAATATGACTGTAACC 540  
DB 730 AACATGACTTGGAAAGATCAAAATTTGAAGAGTGCATGTAATTTTCAATATGACTGTAACC 789  
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTGAGCCCTACTATCTTTTATGCTGTTAATCTGT 600  
DB 790 ATGGTAGCAAACTTAGTACCCCTTCACTGAGCCCTACTATCTTTTATGCTGTTAATCTGT 849  
QY 601 TCTTTGTGTAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660  
DB 850 TCTTTGTGTAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 909  
QY 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTCGCAAT 720  
DB 910 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTCGCAAT 969  
QY 721 TACTTCTGTCCTAATGATATCAGTTTGGAGTTTGGAGTCTCGGAAAACAAACCTGTC 780  
DB 970 TACTTCTGTCCTAATGATATCAGTTTGGAGTTTGGAGTCTCGGAAAACAAACCTGTC 1029  
QY 781 TTTATGTTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCATCTGATT 840  
DB 1030 TTTATGTTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCATCTGATT 1089  
QY 841 TGGGAAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGGTACTGG 900  
DB 1090 TGGGAAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGGTACTGG 1149  
QY 901 GTGAAAGGAGAGAGAGACTTCAATCTCCATAG 930  
DB 1150 GTGAAAGGAGAGAGAGACTTCAATCTCCATAG 1179

RESULT 7  
ADC87038  
ID ADC87038 standard; DNA; 1330 BP.  
XX AC ADC87038;  
XX AC ADC87038;  
DT 01-JAN-2004 (first entry)  
XX Human GPCR gene SEQ ID NO:1491.  
DE ds; gene; human; GPCR;  
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.  
OS Homo sapiens.  
XX EP1270724-A2.  
XX  
XX 02-JAN-2003.  
XX  
XX 18-JUN-2002; 2002EP-00013517.  
XX  
XX 18-JUN-2001; 2001JP-00246789.  
XX  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
XX  
XX Suwa M, Asai K, Akiyama Y, Aburatani H;  
XX  
XX WPI: 2003-315783/31.  
DR P-PSDB; ADC87039.  
XX  
XX New polynucleotide, useful for preparing a composition for treating a  
PT patient in need of increased or suppressed activity or expression of the  
PT guanosine triphosphate-binding protein coupled receptor.  
XX  
XX Claim 1; SEQ ID NO 1491; 28pp; English.  
XX



PT molecule comprises at least 10 contiguous nucleotides, useful for  
PT defining large groups of populations who perceive bitter tastes  
PT differently.  
XX  
PS Claim 1; SEQ ID NO 31; 567bp; English.  
XX  
CC This invention relates to novel human bitter taste receptor (T2R) variant  
CC -specific nucleic acid molecules, each spanning at least one SNP  
CC identified in the specification. Specifically, it refers to the T2R  
CC allele nucleic acid molecules and the encoded proteins thereof. The  
CC present invention describes a method of screening compounds useful for  
CC modulating bitter taste and using a specific binding agent that is  
CC capable of discriminating between two or more polypeptides. Accordingly,  
CC it provides a method of determining the T2R genotype of a subject using  
CC at least one oligonucleotide from each T2R haplotype/allele on a  
CC microarray to identify T2R single nucleotide polymorphisms. As such, the  
CC isolated T2R variant-specific nucleic acid molecules are useful in the  
CC development of flavorings and flavor enhancers as it can be used to  
CC define large groups of populations who perceive bitter tastes  
CC differently. It is also used to identify compounds that interact  
CC differently with different variants of a taste receptor. This  
CC polynucleotide sequence is a bitter taste receptor T2R gene of the  
CC invention.  
XX  
SQ Sequence 930 BP; 253 A; 175 C; 176 G; 316 T; 0 U; 10 Other;  
Query Match 99.4%; Score 924; DB 14; Length 930;  
Best Local Similarity 98.9%; Pred. No. 5.7e-246;  
Matches 918; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTAACCTTTCTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60  
DB 1 ATGTAACCTTTTCTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60  
QY 61 AATTTTGTCTAATAGCTTTATAGCAGCTGGTAATTCATTTGAGTGTTCAGAGACAAAAG 120  
DB 61 AATTTTGTCTAATAGCTTTATAGCAGCTGGTAATTCATTTGAGTGTTCAGAGACAAAAG 120  
QY 121 ATCTCCTTTGTGACCAAAATTCATCTGCTCTGGGGCTTCAGAGTGGTTGCTCTGG 180  
DB 121 ATCTCCTTTGTGACCAAAATTCATCTGCTCTGGGGCTTCAGAGTGGTTGCTCTGG 180  
QY 181 GTATTATTATTAACTGGTATTCACTGTTGTTGAATCCAGCTTTTAAATAGTCTAGAAGTA 240  
DB 181 GTATTATTATTAACTGGTATTCACTGTTGTTGAATCCAGCTTTTAAATAGTCTAGAAGTA 240  
QY 241 AGAAGTCTGCTTATAATATCTGGCAGTGATCAACCAATTTTCAGCAACTGGCTTGTACT 300  
DB 241 AGAAGTCTGCTTATAATATCTGGCAGTGATCAACCAATTTTCAGCAACTGGCTTGTACT 300  
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCGCAATTTCTCAACTTTATTTCTTCAC 360  
DB 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCGCAATTTCTCAACTTTATTTCTTCAC 360  
QY 361 TTAAGAGAGAGAGTTAAGAGTGTCTATCTGGTGATGTTGTTGGGCTTTGCTATTTTG 420  
DB 361 TTAAGAGAGAGAGTTAAGAGTGTCTATCTGGTGATGTTGTTGGGCTTTGCTATTTTG 420  
QY 421 GCTTGTGATCTTTTGTGATAAATGAATGAGATTGTCGCGCAAAAAGAAATTTGAAGA 480  
DB 421 GCTTGTGATCTTTTGTGATAAATGAATGAGATTGTCGCGCAAAAAGAAATTTGAAGA 480  
QY 481 ACATGACTTGAAGATCAAAATGAAGAGTGAATGTACTTTTCAAAATGACTGTAAAC 540  
DB 481 ACATGACTTGAAGATCAAAATGAAGAGTGAATGTACTTTTCAAAATGACTGTAAAC 540  
QY 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCTACTATCTTTATGCTGTTAATCTGT 600  
DB 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCTACTATCTTTATGCTGTTAATCTGT 600  
QY 601 TCTTTGTGTAACATCTCAAGAGATGTCAGCTCCATGGTAAAGGATCTCAAGATCCCAGC 660  
DB 601 TCTTTGTGTAACATCTCAAGAGATGTCAGCTCCATGGTAAAGGATCTCAAGATCCCAGC 660

QY 661 ACCAAGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTCTTGTATGTGCCATT 720  
DB 661 ACSAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTCTTGTATGTGCCATT 720  
QY 721 TACTTTCTGTCCATAATGATATCAGTTTGGAGTCTTGGAAAGTCTTGAAAAACAACCTGTC 780  
DB 721 TACTTTCTGTCCATAATGATATCAGTTTGGAGTCTTGGAAAGTCTTGAAAAACAACCTGTC 780  
QY 781 TTCAATGTTCTGCAAGCTATTAGATTACAGTCTATCCTTCAATCCACCCATTCTCTGATT 840  
DB 781 TTCAATGTTCTGCAAGCTATTAGATTACAGTCTATCCTTCAATCCACCCATTCTCTGATT 840  
QY 841 TGGGGAACACAGAGCTAAAGCAGACTTTTCTTCAGTTTTCGCAATGAGGTACTGG 900  
DB 841 TGGGGAACACAGAGCTAAAGCAGACTTTTCTTCAGTTTTCGCAATGAGGTACTGG 900  
QY 901 GTGAAGGAGAGAGAGACTTTCATCTCCAT 928  
DB 901 GTGAAGGAGAGAGAGACTTTCATCTCCAT 928  
RESULT 9  
ADM33296  
ID ADM33296 standard; cDNA; 927 BP.  
XX  
AC ADM33296;  
XX  
DT 18-NOV-2004 (first entry)  
XX Human bitter taste receptor TAS2R43 encoding cDNA SEQ ID NO:10.  
XX human; bitter taste receptor; food; gene; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 1..927  
FT /\*tag= a  
XX /product= "bitter taste receptor hTAS2R43"  
PN WO2004029087-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-EP010691.  
XX  
PR 25-SEP-2002; 2002US-0413298P.  
XX  
PA (DEER-) DEUT INST ERNAEHRUNGSFORSCHUNG POTSDAM.  
XX  
PI Bufe B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;  
XX  
DR WPI; 2004-305149/28.  
XX P-PSDB; ADM33295.  
XX Novel bitter receptor polynucleotide encoding human TAS2R protein having  
PT bitter substance binding activity, useful for producing nutraceutical or  
PT pharmaceutical compositions comprising antagonists of bitter taste  
PT receptor activity.  
XX  
PS Claim 1; SEQ ID NO 10; 108pp; English.  
XX  
CC The present sequence encodes a human bitter taste receptor. Also  
CC described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)  
CC a vector (II) containing (I); (3) a host cell (III) genetically  
CC engineered with (I) or (II); (4) a transgenic non-human animal (IV)  
CC containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino  
CC acid sequence encoded by (I) or obtained by culturing (III) and  
CC recovering polypeptide; (6) an antibody (VI) specifically binding to (V);  
CC (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an  
CC antagonist/inhibitor (VIII) against (V) which is antibody, the  
CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)

CC isolating (M1) a compound that binds to (V) encoded by (I); (10)  
CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a  
CC foodstuff including human and animal foodstuff, any precursor material or  
CC additive employed in the production of foodstuff comprising (VIII); and  
CC (12) a nutraceutical/pharmaceutical composition comprising (VIII) and an  
CC active agent and optionally a carrier. (III) is useful for producing a  
CC polypeptide encoded by (I), which involves culturing (III) and recovering  
CC the polypeptide encoded by (I). (II) is useful for producing cells  
CC capable of expressing at least one of the bitter taste receptor  
CC polypeptide, which involves genetically cells in vitro with (II), where  
CC the bitter taste receptor polypeptide(s) is(are) encoded by (I). (M1) or  
CC (M2) can be used for producing food or any precursor material or additive  
CC employed in the production of foodstuffs. (M1) or (M2) can also be used  
CC for producing nutraceutical or pharmaceutical compositions. (I), (II),  
CC (VI) or (VIII) can be used for manufacturing a medicament for the  
CC treatment of an abnormally increased or decreased sensitivity towards a  
CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
CC or eliminates bitter tasting components of food and effectively useful in  
CC food industries.

XX SQ Sequence 927 BP; 253 A; 177 C; 179 G; 318 T; 0 U; 0 Other;

Query Match 99.2%; Score 922.2; DB 13; Length 927;  
Best Local Similarity 99.7%; Pred. No. 1.8e-245;  
Matches 924; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCAATTTTCCAGTCTGTGTAGTGTACATTTGTTATTGGA 60  
Db 1 ATGATAACTTTTCTACCCATCAATTTTCCAGTCTGTGTAGTGTACATTTGTTATTGGA 60  
QY 61 AATTTTGCTAATGGCTTCATAGCAGCTGTTAAATTCATTGAGTGGTTCAAGACAAAAAG 120  
Db 61 AATTTTGCTAATGGCTTCATAGCAGCTGTTAAATTCATTGAGTGGTTCAAGACAAAAAG 120  
QY 121 ATCTCTTTGCTGACCAAAATTCCTACTGCTCTGCGGCTCTCCAGAGTGGTTTGTCTCG 180  
Db 121 ATCTCTTTGCTGACCAAAATTCCTACTGCTCTGCGGCTCTCCAGAGTGGTTTGTCTCG 180  
QY 181 GTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAGTA 240  
Db 181 GTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAGTA 240  
QY 241 AGAAGTACTGTTTAAATATCTGGGAGTGTATCAACATTTGAGCACTGGCTGTACT 300  
Db 241 AGAAGTACTGTTTAAATATCTGGGAGTGTATCAACATTTGAGCACTGGCTGTACT 300  
QY 301 ACCCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCCAACTTTATTTTCTTCAC 360  
Db 301 ACCCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCCAACTTTATTTTCTTCAC 360  
QY 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGTTGATGTTTGGGCTTTTGTCTATTTTGG 420  
Db 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGTTGATGTTTGGGCTTTTGTCTATTTTGG 420  
QY 421 GCTTGTCTATTTTGTGATAAATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
Db 421 GCTTGTCTATTTTGTGATAAATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
QY 481 AACATCAGTTTGAAGATCAAAATGAAGAGTGCATCTCTTTTCAATATGATGATGATGAT 540  
Db 481 AACATCAGTTTGAAGATCAAAATGAAGAGTGCATCTCTTTTCAATATGATGATGATGAT 540  
QY 541 ATGGTAGCAAACTTAGTACCTTTCACTCTGACCTACTATCTTTTATGCTGTTTAACTCT 600  
Db 541 ATGGTAGCAAACTTAGTACCTTTCACTCTGACCTACTATCTTTTATGCTGTTTAACTCT 600  
QY 601 TCTTTGTGTAACATCTCAAGAGATGCGCTCCATGGTAAAGGATCTCAAGATCCCGC 660  
Db 601 TCTTTGTGTAACATCTCAAGAGATGCGCTCCATGGTAAAGGATCTCAAGATCCCGC 660  
QY 661 ACCAAGGTCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
Db 661 ACCAAGGTCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 720

QY 721 TACTTTCTCTCCATATGATATCAGTTTGGAGTCTTGGAGTCTGGAACCAACCACTGTC 780  
Db 721 TACTTTCTCTCCATATGATATCAGTTTGGAGTCTTGGAGTCTGGAACCAACCACTGTC 780  
QY 781 TTCAATGTTCTGCAAGAGCTATTAGATTTCAGCTATCTTCAATCCACCATTTCATCTGATT 840  
Db 781 TTCAATGTTCTGCAAGAGCTATTAGATTTCAGCTATCTTCAATCCACCATTTCATCTGATT 840  
QY 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTCTTCTTGGCAAAATGAGGTACTGG 900  
Db 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTCTTCTTGGCAAAATGAGGTACTGG 900  
QY 901 GTGGAAGGAGAGAGACTTTCATCTCCA 927  
Db 901 GTGGAAGGAGAGAGACTTTCATCTCCA 927  
RESULT 10  
ADW74575  
ID ADW74575 standard; DNA; 930 BP.  
XX AC ADW74575;  
XX DT 07-APR-2005 (first entry)  
XX DE Human bitter taste receptor haplotype gene T2R44 Seq 187.  
XX KW SNP detection; SNP; single nucleotide polymorphism; screening;  
XX KW DNA microarray; flavor enhancer; ds; gene.  
XX OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..930  
FT /tag= a  
FT /product= "T2R protein"  
FT /replace(103,c)  
FT /tag= b  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(484,t)  
FT /tag= c  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(599,a)  
FT /tag= d  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(649,g)  
FT /tag= e  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(656,t)  
FT /tag= f  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(680,c)  
FT /tag= g  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(718,g)  
FT /tag= h  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(827,g)  
FT /tag= i  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /replace(843,t)  
FT /tag= j  
FT /standard\_name= "Single nucleotide polymorphism"  
XX WO2005007891-A2.  
XX 27-JAN-2005.  
XX 18-JUN-2004; 2004WO-US019489.  
XX 19-JUN-2003; 2003US-0480035P.  
XX



(USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Drayna D, Kim U;

XX WPI; 2005-152091/16.

DR P-PSDB; ADW74576.

XX New isolated bitter taste receptor (T2R) variant-specific nucleic acid molecule comprises at least 10 contiguous nucleotides, useful for defining large groups of populations who perceive bitter tastes differently.

PS Claim 9; SEQ ID NO 187; 567pp; English.

XX This invention relates to novel human bitter taste receptor (T2R) variant -specific nucleic acid molecules, each spanning at least one SNP identified in the specification. Specifically, it refers to the T2R allele nucleic acid molecules and the encoded proteins thereof. The present invention describes a method of screening compounds useful for modulating bitter taste and using a specific binding agent that is capable of discriminating between two or more polypeptides. Accordingly, it provides a method of determining the T2R genotype of a subject using at least one oligonucleotide from each T2R haplotype/allele on a microarray to identify T2R single nucleotide polymorphisms. As such, the isolated T2R variant-specific nucleic acid molecules are useful in the development of flavorings and flavor enhancers as it can be used to define large groups of populations who perceive bitter tastes differently. It is also used to identify compounds that interact differently with different variants of a taste receptor. This polynucleotide sequence is a bitter taste receptor T2R haplotype gene of the invention.

XX Sequence 930 BP; 246 A; 177 C; 192 G; 315 T; 0 U; 0 Other;

Query Match 91.7%; Score 852.8; DB 14; Length 930;

Best Local Similarity 94.9%; Pred. No. 3.4e-226;

Matches 881; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ATGATTAACCTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60  
DB |||||  
QY 1 ATGACAACTTTTATACCCATCATTTTTTCCAGTCTGGTAGTGGTTCTATTGTTATTGGA 60  
DB |||||  
QY 61 AATTTTGTCAATGGCTTCATAGCAGCTGTAATTCATTGAGTGGTTCAAGAGACAAAG 120  
DB |||||  
QY 61 AATTTTGTCAATGGCTTCATAGCAGTGGTAATTCATTGAGTGGTCAAGAGACAAAG 120  
DB |||||  
QY 121 ATCTCTTTTGTGACCAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180  
DB |||||  
QY 121 ATCTCTTTTGTGACCAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180  
DB |||||  
QY 181 GTATTATTATTAACCTGGTATTCAACTGTGTTGAATCCAGCTTTTATAGTGTAGAAGTA 240  
DB |||||  
QY 181 GTATTATTATTAATTTGGTATTCAACTGTGTTTAATCCAGCTTTTATAGTGTAGAAGTA 240  
DB |||||  
QY 241 AGAATCTACTGCTTATATATCTGGGAGTGATCAACCATTTTCAGCAACTGGCTTGGTACT 300  
DB |||||  
QY 241 AGAATCTACTGCTTATATATCTGGGAGTGATCAACCGGCATTTTCAGCAACTGGCTTGGTACT 300  
DB |||||  
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACTTTATTTTCTTCAC 360  
DB |||||  
QY 301 AGCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAACTTTATTTTCTTCAC 360  
DB |||||  
QY 361 TTAAGAGAGAGATTAAAGAGTGTCTCTGGTGTGTTGTTGGGCTTTGCTATTATTG 420  
DB |||||  
QY 361 TTAAGAGAGAGATTAAAGAGTGTCTCTGGTGTGTTGTTGGGCTTTTACTATTATTG 420  
DB |||||  
QY 421 GCTTGTCTATCTTTTGTGATAACATGAATGAGATTGTGGGACAAAGAAATTTGAAGA 480  
DB |||||  
QY 421 GCTTGTCAACTTTTCTGATTAACATGAAGAGATTGTACGGACAAAGAAATATGAAGA 480  
DB |||||  
QY 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGCATGTACTTTTCAAAATATGACTGTAACC 540  
DB |||||  
QY 481 AACATGACTTGGAGATCAAAATTTGAGGAGTGCAGTGTACCTTTTCAGATCGAGCTGTAACC 540  
DB |||||

XX The invention relates to a mammalian taste cell-specific G protein-  
CC coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste  
CC sensation. The T2R polypeptides and their associated polynucleotides are  
CC useful for screening one or more compounds for the presence of taste  
CC detectable by a mammal. Modulators of T2R polypeptides (modulators of  
CC taste transduction) are useful for pharmacological and genetic  
CC modulations of taste signalling pathways. These modulatory compounds are  
CC then used in food and pharmaceutical industries to customise taste, e.g.,  
CC to decrease or mask the bitter taste of foods or drugs. This sequence  
CC represents cDNA encoding the human T2R64 (hrT2R64) polypeptide  
XX  
SQ Sequence 930 BP; 244 A; 179 C; 193 G; 314 T; 0 U; 0 Other;

Query Match 91.6%; Score 851.6; DB 6; Length 930;  
Best Local Similarity 94.7%; Pred. No. 7.2e-226;  
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTCAGTCTGGTAGTGGTTACATTGTTATTGGA 60  
DB 1 ATGCAAACTTTTATACCCATCATTTTTCAGTCTGGTAGTGGTTCTATTGTTATTGGA 60  
QY 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120  
DB 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120  
QY 121 ATCTCTTTGTGACAAATTCCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180  
DB 121 ATCTCTTTGTGACAGATTCCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180  
QY 181 GTATTATTATTAACCTGTTTCACTGTTGTTGAATCCAGCTTTTAATAGTGTAGAATA 240  
DB 181 GTATTATTATTAACCTGTTTCACTGTTGTTGAATCCAGCTTTTAATAGTGTAGAATA 240  
QY 241 AGAACTACTGCTTATAATATCTGGCAGTGATCAACCACTTTCAGCAACTGGCTCTACT 300  
DB 241 AGAACTACTGCTTATAATATCTGGCAGTGATCAACCACTTTCAGCAACTGGCTCTACT 300  
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCAACTTTATTTTCTTCAC 360  
DB 301 AGCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCAACTTTATTTTCTTCAC 360  
QY 361 TTAAGAGAGAGTTAAGAGTGTCACTCTGGTAGTGGTTGGGCGCTTGTCTATTTTG 420  
DB 361 TTAAGAGAGAGTTAAGAGTGTCACTCTGGTAGTGGTTGGGCGCTTGTCTATTTTG 420  
QY 421 GCTTGTCTATCTTTTGTGATAAATGAATGATGATGTCGCGACAAAAGAAATTTGAAGA 480  
DB 421 GCTTGTCTATCTTTTGTGATAAATGAATGATGATGTCGCGACAAAAGAAATTTGAAGA 480  
QY 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGCATATGTACTTTTCAAAATATGACTGTAA 540  
DB 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGCATATGTACTTTTCAAAATATGACTGTAA 540  
QY 541 ATGTAGCAAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTATATCTGT 600  
DB 541 ACCTAGGAAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTATATCTGT 600  
QY 601 TCTTTGTGAACATCTCAAGAGATGCAGTCCATGTTGAAGATCTCAAGATCCAGC 660  
DB 601 TCTTTGTGAACATCTCAAGAGATGCAGTCCATGTTGAAGATCTCAAGATCCAGC 660  
QY 661 ACCAAGTCCACATAAAAGCTTTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
DB 661 ACCAAGTCCACATAAAAGCTTTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
QY 721 TACTTTCTGTCCATTAATGATATCAGTTTGGAGTTTGGAAAGTCTGGAAAAAACAACCTGTC 780  
DB 721 TACTTTCTGTCCATTAATGATATCAGTTTGGAGTTTGGAGTCTGGAAAAAACAACCTGTC 780  
QY 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCTCTCAATCCACCTTATCTCTGATT 840  
DB 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCTCTCAATCCACCTTATCTCTGATT 840

QY 841 TGGGAAAACAAGAGCTAAAGCAGACTTTTCTTCAGTTTTCGCAATGAGGTACTGG 900  
DB 841 TGGGAAAACAAGAGCTAAAGCAGACTTTTCTTCAGTTTTCGCGCAAGTGAGGTACTGG 900  
QY 901 GTGAAGGAGAGAGAGACTTCATCTCCATAG 930  
DB 901 GTGAAGGAGAGAGAGCCCTTCATCTCCATAG 930

## RESULT 12

ABZ43215

ID ABZ43215 standard; DNA; 930 BP.

XX AC

XX ABZ43215;

XX DT 06-MAR-2003 (first entry)

XX Human GPCR polynucleotide SEQ ID NO 691.

XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;  
KW drug development; gustatory; taste; fragrance; gene; ds.  
XX Homo sapiens.

XX WO200216548-A2.

XX 28-FEB-2002.

XX 30-JUL-2001; 2001WO-1B001446.

XX 04-AUG-2000; 2000JP-00237818.

XX 13-FEB-2001; 2001JP-00034434.

XX (NISC-) JAPAN SCI &amp; TECHNOLOGY CORP.

XX Haga T, Takeda S, Mitaku S;

XX WPI; 2002-304118/34.

XX P-PSDB; ABP95941.

PT Database global search for G protein-coupled receptors, proteins and  
PT encoded genes for studying in vivo signal transduction mechanism and  
PT identifying targets for drug development.  
XX Claim 9; SEQ ID NO 691; 97pp + Sequence Listing; Japanese.

XX The invention relates to a method for screening G protein-coupled  
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-  
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane  
CC domains with 250-1000 amino acid residues to give a gene homologous with  
CC a known GPCR gene. The receptor proteins and encoded genes are useful for  
CC studying in vivo signal transduction mechanism and identifying targets  
CC for drug development e.g. based on olfactory and gustatory receptors in  
CC form of agonists and antagonists by screening intrinsic and extrinsic  
CC ligands as bitter taste inhibitors, taste enhancers and fragrance  
CC improvers. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 930 BP; 244 A; 179 C; 193 G; 314 T; 0 U; 0 Other;

Query Match 91.6%; Score 851.6; DB 6; Length 930;

Best Local Similarity 94.7%; Pred. No. 7.2e-226;

Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTCAGTCTGGTAGTGGTTACATTGTTATTGGA 60

DB 1 ATGCAAACTTTTATACCCATCATTTTTCAGTCTGGTAGTGGTTCTATTGTTATTGGA 60

QY 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120

DB 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120

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QY 121 ATCTCCTTTGCTGACCAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180
Db |||||
QY 121 ATCTCCTTTTGTGACCAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180
Db |||||
QY 181 GTATTATTATAAATCTGATTTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
QY 181 GTATTATTATAAATCTGATTTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGATCAACCAATTTCAAGCACTGGCTGCTACT 300
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGATCAACCAATTTCAAGCACTGGCTGCTACT 300
Db |||||
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGAATTTCTCAACTTTATTTTCTTCCAC 360
Db |||||
QY 301 AGCCTCAGCATATTTTATTTGCTCAAGATTCGAATTTCTCAACTTTATTTTCTTCCAC 360
Db |||||
QY 361 TTAAGAGGAGATTTAAGAGTGCTAATCTGTGATGTTGTTGGGCGCTTTGCTATTTTG 420
Db |||||
QY 361 TTAAGAGGAGATTTAAGAGTGCTAATCTGTGATGTTGTTGGGCGCTTTTACTATTTTG 420
Db |||||
QY 421 GCTTGTCTATCTTTTGTGTATTAACATGAATGAGATTTGGGACAAAAAGAAATTTGAAGGA 480
Db |||||
QY 421 GCTTGTCAACTTTTGTGTATTAACATGAAGAGATTTGACGACAAAAAGAAATTTGAAGGA 480
Db |||||
QY 481 AACATGACTTGAAGATCAAAATTTGAAGTGCATGTTTCCAAATGACTGTAAACC 540
Db |||||
QY 481 AACTTGACTTGAAGATCAAAATTTGAAGTGCATGTTTCCAAATGACTGTAAACC 540
Db |||||
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATCTGTTAATCTGT 600
Db |||||
QY 541 ACGCTAGGAACTTAGTACCCCTTCACTCTGACCCCTGCTATGTTTTCGTTGTTAATCTGT 600
Db |||||
QY 601 TCTTTGTGTAAACATCTCAAGAAGATGAGCTTCATGTGTAAAGATCTCAAGATCCCAGC 660
Db |||||
QY 601 TCTCTGTGTAAACATCTCAAGAAGATGAGCTTCATGTGTAAAGATCTCAAGATCCCAGC 660
Db |||||
QY 661 ACCAGGTCCCATAAAGCTTTGCAAACTGTGATCTCTTCCCTCTGTTATGTGCCATT 720
Db |||||
QY 661 ACCAAGGTCCCATAAAGCTTTGCAAACTGTGATCTCTTCCCTCTGTTATGTGCCATT 720
Db |||||
QY 721 TACTTTCTGTCATATGATATCACTTTGGAGTTTGGAAAGTCTCGGAAACAAACCTGTC 780
Db |||||
QY 721 TACTTTCTGTCATATGATATCACTTTGGAGTTTGGAGTCTCGGAAACAAACCTGTC 780
Db |||||
QY 781 TTCATGTTCTGAAAGCTATTAGATTCAGCTATCCCTTCAATCCACCCATTCATCTGATT 840
Db |||||
QY 781 TTCATGTTCTGAAAGCTATTAGATTCAGCTATCCCTTCAATCCACCCATTCATCTGATT 840
Db |||||
QY 841 TGGGGAACAAAGACTTAAGCAGACTTTTCTTTCAGTTTTCGCAAAATGAGGTACTGG 900
Db |||||
QY 841 TGGGGAACAAAGACTTAAGCAGACTTTTCTTTCAGTTTTCGCAAAATGAGGTACTGG 900
Db |||||
QY 901 GTGAAAGGAGAGAACTTCATCTCCATAG 930
Db |||||
QY 901 GTGAAAGGAGAGAACTTCATCTCCATAG 930
Db |||||
```

RESULT 13

```
ACC44476
ID ACC44476 standard; DNA; 930 BP.
XX
AC ACC44476;
XX
XX 25-JUL-2003 (first entry)
XX
XX Gene encoding human GI endocrine cell specific GPCR GT2R-h55.
XX
KW Chemosensor; G-protein coupled receptor; gene; ds; GPCR; receptor;
XX gastrointestinal tract; taste; ion channel; enteroendocrine cell.
XX
OS Homo sapiens.
XX
```

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PN WO2003031604-A1.
XX 17-APR-2003.
XX 11-OCT-2002; 2002WO-US032664.
XX 12-OCT-2001; 2001US-0328993P.
XX (REGC ) UNIV CALIFORNIA.
PA (PHLE/) PHLEGER C S W.
XX Walsh JH, Rozengurt JE, Wu SV;
XX WPI; 2003-381713/36.
DR P-PSDB; ABR58040.
XX
PT New nucleic acid encoding a chemosensing G-protein coupled receptor,
PT useful for identifying chemical sensing receptors and signaling molecules
PT that allow pharmacological and genetic modulation of taste transduction
PT pathways.
XX
PS Claim; Page 93; 101pp; English.
XX
CC This sequence represents a gene encoding a novel isolated chemosensing G-
CC protein coupled receptor (GPCR) from the gastrointestinal tract. The
CC nucleic acid is useful for identifying or isolating chemical sensing
CC receptors (including taste ion channels) and signaling molecules that
CC would allow pharmacological and genetic modulation of taste transduction
CC pathways. The native STC-1 enteroendocrine cells that naturally express
CC GT2R are useful in identifying modulators of taste receptor-mediated
CC signal transduction. These cells are also used as models for studying
CC taste-mediated signal transduction
XX
SQ Sequence 930 BP; 244 A; 179 C; 193 G; 314 T; 0 U; 0 Other;
Query Match 91.6%; Score 851.6; DB 8; Length 930;
Best Local Similarity 94.7%; Pred. No. 7.2e-226;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1 ATGATAACTTTTTCACCATCATTTTTTCCAGTCTGGTAGTGGTTTACATTTGTTATTGGA 60
Db |||||
QY 61 AATTTTGTCTAATGCTTCATAGCACTGTAATTCATTGAGTGTCCAGAGACAAAG 120
Db |||||
QY 61 AATTTTGTCTAATGCTTCATAGCACTGTAATTCATTGAGTGTCCAGAGACAAAG 120
Db |||||
QY 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG 180
Db |||||
QY 181 GTATTATTATAAATCTGATTTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGATCAACCAATTTCAAGCACTGGCTGCTACT 300
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGATCAACCAATTTCAAGCACTGGCTGCTACT 300
Db |||||
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCCAAATTTCTCAACTTTTCTTCCAC 360
Db |||||
QY 361 TTAAGAGGAGATTTAAGAGTGCTAATCTGTGATGTTGTTGGGCGCTTTGCTATTTTG 420
Db |||||
QY 421 GCTTGTCTATCTTTTGTGATAAACATGAATGAGATTTGGGACAAAAAGAAATTTGAAGGA 480
Db |||||
QY 421 GCTTGTCAACTTTTGTGATAAACATGAAGAGATTTGACGACAAAAAGAAATTTGAAGGA 480
Db |||||
QY 481 AACATGACTTGAAGATCAAAATTTGAAGTGCATGTTTCCAAATGACTGTAAACC 540
Db |||||
QY 481 AACTTGACTTGAAGATCAAAATTTGAAGTGCATGTTTCCAAATGACTGTAAACC 540
Db |||||
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATCTGTTAATCTGT 600
Db |||||
QY 541 ACGCTAGGAACTTAGTACCCCTTCACTCTGACCCCTGCTATGTTTTCGTTGTTAATCTGT 600
Db |||||
QY 601 TCTTTGTGTAAACATCTCAAGAAGATGAGCTTCATGTGTAAAGATCTCAAGATCCCAGC 660
Db |||||
QY 601 TCTCTGTGTAAACATCTCAAGAAGATGAGCTTCATGTGTAAAGATCTCAAGATCCCAGC 660
Db |||||
QY 661 ACCAGGTCCCATAAAGCTTTGCAAACTGTGATCTCTTCCCTCTGTTATGTGCCATT 720
Db |||||
QY 661 ACCAAGGTCCCATAAAGCTTTGCAAACTGTGATCTCTTCCCTCTGTTATGTGCCATT 720
Db |||||
QY 721 TACTTTCTGTCATATGATATCACTTTGGAGTTTGGAAAGTCTCGGAAACAAACCTGTC 780
Db |||||
QY 721 TACTTTCTGTCATATGATATCACTTTGGAGTTTGGAGTCTCGGAAACAAACCTGTC 780
Db |||||
QY 781 TTCATGTTCTGAAAGCTATTAGATTCAGCTATCCCTTCAATCCACCCATTCATCTGATT 840
Db |||||
QY 781 TTCATGTTCTGAAAGCTATTAGATTCAGCTATCCCTTCAATCCACCCATTCATCTGATT 840
Db |||||
QY 841 TGGGGAACAAAGACTTAAGCAGACTTTTCTTTCAGTTTTCGCAAAATGAGGTACTGG 900
Db |||||
QY 841 TGGGGAACAAAGACTTAAGCAGACTTTTCTTTCAGTTTTCGCAAAATGAGGTACTGG 900
Db |||||
QY 901 GTGAAAGGAGAGAACTTCATCTCCATAG 930
Db |||||
QY 901 GTGAAAGGAGAGAACTTCATCTCCATAG 930
Db |||||
```



Db 781 TTCATGTTCTGCAAGCTATTAGATTACAGTATCTTCAATCCACCCCAATTCATCTCGATT 840  
Qy 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGGTACTGG 900  
Db 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCGGCAAGTGAGGTACTGG 900  
Qy 901 GTGAAGGAGAGAGAGCTTCACTCTCCATAG 930  
Db 901 GTGAAGGAGAGAGAGCTTCACTCTCCATAG 930

## RESULT 15

ADD18119

ID ADD18119 standard; DNA; 971 BP.

XX

AC ADD18119;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human G-protein coupled receptor (GPCR) DNA sequence Seq ID5.

XX

KW G protein coupled receptor; GPCR; signal transduction pathway; G protein;  
KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;  
KW colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;  
KW sleeplessness; hypertension; anxiety; stress; renal failure;  
KW cardiovascular disorder; neural disorder; oncology disorder;  
KW immune disorder; neuroprotective; gene therapy; gene; ds.

OS Homo sapiens.  
XX

XX FH Key Location/Qualifiers  
XX CDS 20..949

XX FT /\*tag= a

XX FT /product= "Human G-protein coupled receptor"

XX PN WO2003016478-A2.

XX

XX PD 27-FEB-2003.

XX

XX PF 15-AUG-2002; 2002WO-US026017.

XX

XX PR 20-AUG-2001; 2001US-03136588.

XX PR 12-SEP-2001; 2001US-0318675P.

XX PR 30-OCT-2001; 2001US-0340703P.

XX PR 26-NOV-2001; 2001US-0333417P.

XX PR 06-DEC-2001; 2001US-0338367P.

XX PR 06-FEB-2002; 2002US-0355596P.

XX

XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX

XX PI Feder JN, Ramanathan CS, Gopal S, Mintier GA;

XX

XX DR WPI; 2003-278558/27.

XX

XX DR P-PSDB; ADD18022.

XX

PT New nucleic acid, useful for manufacturing a medicament for preventing,  
PT treating or ameliorating a medical condition e.g., neural disorder.

XX

XX PS Example 2; SEQ ID NO 5; 251pp; English.

XX

CC This invention relates to novel G protein coupled receptors (GPCRs) and  
CC their encoding nucleotide sequences. Many medically significant  
CC biological processes are mediated by proteins participating in signal  
CC transduction pathways involving G proteins. GPCRs are one of the largest  
CC receptor superfamilies known. These receptors are biologically important  
CC and malfunction of these receptors results in diseases such as  
CC Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal  
CC pigmentosa and arthritis. They are also involved in depression,  
CC schizophrenia, sleeplessness, hypertension, anxiety, stress, renal  
CC failure and other cardiovascular, neural, oncology and immune disorders.  
CC A modulator of the GPCRs of the invention may have neuroprotective  
CC activity whilst the sequences of the invention may be useful for gene  
CC therapy. The invention may also be useful for manufacturing a medicament

Search completed: May 1, 2006, 07:30:18  
Job time : 621 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:12:56 ; Search time 140 Seconds  
(without alignments)  
969.772 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MTFPLPIPFSSILVVFVIG.....FLSVFQWRYWVGKGTSSP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1597	100.0	309	5	AAU11384	AAU11384 Human T2R
2	1597	100.0	309	5	ABP95936	ABP95936 Human GPC
3	1597	100.0	309	6	ABP97669	ABP97669 Amino aci
4	1597	100.0	309	6	ABR58042	ABR58042 Human GI
5	1597	100.0	309	7	ADC87039	ADC87039 Human GPC
6	1597	100.0	309	8	ADR29240	ADR29240 Taste rec
7	1575	98.6	309	8	ADM33295	ADM33295 Human bit
8	1518	95.1	309	9	ADW74420	ADW74420 Human bit
9	1440	90.2	309	5	AAU11390	AAU11390 Human T2R
10	1440	90.2	309	6	ABR58039	ABR58039 Human GI
11	1440	90.2	309	7	ADC87131	ADC87131 Human GPC
12	1440	90.2	309	8	ADR29252	ADR29252 Taste rec
13	1440	90.2	309	9	ADW74596	ADW74596 Human bit
14	1438	90.0	309	9	ADW74594	ADW74594 Human bit
15	1438	90.0	309	9	ADW74576	ADW74576 Human bit
16	1427	89.4	309	8	ADM33297	ADM33297 Human bit
17	1427	89.4	309	9	ADW74582	ADW74582 Human bit
18	1426	89.3	309	9	ADW74578	ADW74578 Human bit
19	1424	89.2	309	5	AAU11386	AAU11386 Human T2R
20	1424	89.2	309	5	ABP95941	ABP95941 Human GPC
21	1424	89.2	309	6	ABR58040	ABR58040 Human GI
22	1424	89.2	309	7	ADC87041	ADC87041 Human GPC
23	1424	89.2	309	7	ADD18022	ADD18022 Human G-p
24	1424	89.2	309	8	ADR29244	ADR29244 Taste rec

25	1424	89.2	309	9	ADW74584	Adw74584 Human bit
26	1414	88.5	309	9	ADW74586	Adw74586 Human bit
27	1413	88.5	309	9	ADW74588	Adw74588 Human bit
28	1410	88.3	309	9	ADW74580	Adw74580 Human bit
29	1406	88.0	299	8	ADM33301	Adm33301 Human bit
30	1375	86.1	299	9	ADW74424	Adw74424 Human bit
31	1371	85.8	299	9	ADW74422	Adw74422 Human bit
32	1348	84.4	299	4	AAB87780	Aab87780 Human T2R
33	1348	84.4	299	5	ABP95930	Abp95930 Human GPC
34	1348	84.4	299	6	ABR58035	AbR58035 Human GI
35	1348	84.4	299	7	ADC87027	Adc87027 Human GPC
36	1348	84.4	299	8	ADR29137	Adr29137 Taste rec
37	1345	84.2	287	9	ADW74598	Adw74598 Human bit
38	1335	83.6	299	8	ADM33299	Adm33299 Human bit
39	1299	81.3	308	8	ADM33303	Adm33303 Human bit
40	1299	81.3	309	9	ADW74426	Adw74426 Human bit
41	1299	81.3	319	6	ABR58034	AbR58034 Human GI
42	1299	81.3	319	7	ADC87029	Adc87029 Human GPC
43	1299	81.3	319	9	ADW74604	Adw74604 Human bit
44	1293	81.0	319	4	AAB87774	Aab87774 Human T2R
45	1293	81.0	319	5	ABP95929	Abp95929 Human GPC

## ALIGNMENTS

### RESULT 1

AAU11384

ID AAU11384 standard; protein; 309 AA.

XX AC AAU11384;

XX DT 26-MAR-2002 (first entry)

XX DE Human T2R61 (ht2R61) polypeptide.

XX KW Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor;

XX KW ht2R61; T2R61; T2R; bitter taste sensation; taste signalling pathway;

XX KW taste transduction; food taste masking; drug taste masking.

XX OS Homo sapiens.

XX PN WO200177676-A1.

XX PD 18-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010739.

XX PR 07-APR-2000; 2000US-0195532P.

XX PR 13-NOV-2000; 2000US-0247014P.

(SENO-) SENOMTX INC.

PI Adler JE;

XX WPI; 2002-017486/02.

XX N-PSDB; AAS18167.

Novel isolated mammalian taste cell-specific G protein-coupled receptor, T2R, involved in bitter taste sensation, useful for identifying taste modulators that are used to decrease or mask bitter taste of foods or drugs.

Claim 60; Page 72; 103pp; English.

The invention relates to a mammalian taste cell-specific G protein-coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste sensation. The T2R polypeptides and their associated polynucleotides are useful for screening one or more compounds for the presence of taste detectable by a mammal. Modulators of T2R polypeptides (modulators of taste transduction) are useful for pharmacological and genetic modulations of taste signalling pathways. These modulatory compounds are then used in food and pharmaceutical industries to customise taste, e.g.,

CC to decrease or mask the bitter taste of foods or drugs. This sequence  
 CC represents the human T2R61 (hT2R61) polypeptide  
 XX  
 SQ Sequence 309 AA;

Query Match 100.0%; Score 1597; DB 5; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-152; Indels 0; Gaps 0;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60  
 DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLKIANFSNFIPLH 120  
 DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLVMLLGSLCSLCKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 180  
 DB 121 LKRRVKSIVLVMLLGSLCSLCKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 180

QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240  
 DB 181 MVANLVPFTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTVISFVQMRYW 300  
 DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTVISFVQMRYW 300

QY 301 VKGEKTSSP 309  
 DB 301 VKGEKTSSP 309

RESULT 2  
 ABP95936  
 ID ABP95936 standard; protein; 309 AA.  
 XX  
 AC ABP95936;  
 XX  
 DT 06-MAR-2003 (first entry)  
 XX  
 DE Human GPCR polypeptide SEQ ID NO 682.  
 XX  
 KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;  
 KW drug development; gustatory; taste; fragrance; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200216548-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 30-JUL-2001; 2001WO-IB001446.  
 XX  
 PR 04-AUG-2000; 2000JP-00237818.  
 PR 13-FEB-2001; 2001JP-00034434.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Haga T, Takeda S, Mitaku S;  
 XX  
 DR WPI; 2002-304118/34.  
 DR N-PSDB; AB243210.  
 XX  
 PT Database global search for G protein-coupled receptors, proteins and  
 PT encoded genes for studying in vivo signal transduction mechanism and  
 PT identifying targets for drug development.  
 XX  
 XX Claim 10; SEQ ID NO 682; 97pp + Sequence Listing; Japanese.  
 PS  
 XX The invention relates to a method for screening G protein-coupled  
 CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP959596-  
 CC

CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane  
 CC domains with 250-1000 amino acid residues to give a gene homologous with  
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for  
 CC studying in vivo signal transduction mechanism and identifying targets  
 CC for drug development e.g. based on olfactory and gustatory receptors in  
 CC form of agonists and antagonists by screening intrinsic and extrinsic  
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance  
 CC improvers. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 309 AA;

Query Match 100.0%; Score 1597; DB 5; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-152; Indels 0; Gaps 0;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60  
 DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLKIANFSNFIPLH 120  
 DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLVMLLGSLCSLCKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 180  
 DB 121 LKRRVKSIVLVMLLGSLCSLCKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 180

QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240  
 DB 181 MVANLVPFTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTVISFVQMRYW 300  
 DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTVISFVQMRYW 300

QY 301 VKGEKTSSP 309  
 DB 301 VKGEKTSSP 309

RESULT 3  
 ABP97669  
 ID ABP97669 standard; protein; 309 AA.  
 XX  
 AC ABP97669;  
 XX  
 DT 16-MAY-2003 (first entry)  
 XX  
 DE Amino acid sequence of human T2R61 polypeptide.  
 XX  
 KW Human; T2R4; G protein coupled receptor; GPCR; taste receptor;  
 KW bitter alkaloid quinine; denatonium; 6-nitrosaccharin; T2R44; T2R61;  
 KW bitter taste; saccharin.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003006482-A2.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 10-JUL-2002; 2002WO-US021602.  
 XX  
 PR 10-JUL-2001; 2001US-0303811P.  
 PR 15-APR-2002; 2002US-0372089P.  
 XX  
 PA (SENO-) SENOMYX INC.  
 XX  
 PI Pronin A, Connor J, Tang H, Keung W, Servant G, Adler JB;  
 PI O'Connell S, Brust P;  
 XX  
 DR WPI; 2003-221711/21.

DR N-PSDB; ABZ68712.  
XX  
PT Assay method for identifying a compound, which modulates hT2R4 associated  
PT bitter taste, involves screening a compound for its effect on quinine or  
PT a structurally related compound to induce activation of hT2R4.  
XX  
PS Claim 35; Page 11; 82pp; English.  
XX  
CC The present sequence is a human T2R61 protein. T2R61 is a G protein  
CC coupled receptor (GPCR) that is specifically activated by the bitter  
CC derivative of saccharin, 6-nitrosaccharin. T244 is activated by  
CC denatonium and 6-nitrosaccharin. T2R4 is activated by the bitter alkaloid  
CC quinine. The specification describes an assay for identifying compounds  
CC which modulate T2R4, T2R61 and T2R44 associated bitter taste. The  
CC identified compounds are used in foods, beverages and medicines to  
CC inhibit bitter taste e.g. saccharin containing diet beverages, foods or  
CC medicinal products  
XX  
SQ Sequence 309 AA;  
Query Match 100.0%; Score 1597; DB 6; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.2e-152;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MITPLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
DB 1 MITPLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
QY 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFSNWLATLISIFYLLKIANFSNFIPLH 120  
DB 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFSNWLATLISIFYLLKIANFSNFIPLH 120  
QY 121 LKRRVKSIVLVMLLGPLEFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
DB 121 LKRRVKSIVLVMLLGPLEFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
QY 181 MVANLVPFTLLTLLSFMLLICSCLKHLKQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
DB 181 MVANLVPFTLLTLLSFMLLICSCLKHLKQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFILSVFWMRYW 300  
DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFILSVFWMRYW 300  
QY 301 VKGEKTSSP 309  
DB 301 VKGEKTSSP 309  
RESULT 4  
ABR58042  
ID ABR58042 standard; protein; 309 AA.  
XX  
AC ABR58042;  
XX  
DT 25-JUL-2003 (first entry)  
XX  
DE Human GI endocrine cell specific GPCR GT2R-h57.  
XX  
KW Chemosensor; G-protein coupled receptor; GPCR; receptor; ion channel;  
KW gastrointestinal tract; taste; enteroendocrine cell.  
XX  
OS Homo sapiens.  
XX  
PN WO2003031604-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032664.  
XX  
PR 12-OCT-2001; 2001US-0328993P.  
XX  
PA (REGC ) UNIV CALIFORNIA.

PA (PHLE/) PHLEGER C S W.  
XX  
PI Walsh JH, Rozengurt JE, Wu SV;  
XX  
DR WPI; 2003-381713/36.  
DR N-PSDB; ACC44478.  
XX  
PT New nucleic acid encoding a chemosensing G-protein coupled receptor,  
PT useful for identifying chemical sensing receptors and signaling molecules  
PT that allow pharmacological and genetic modulation of taste transduction  
PT pathways.  
XX  
PS Disclosure; Page 96-97; 101pp; English.  
XX  
CC This sequence represents a novel isolated chemosensing G-protein coupled  
CC receptor (GPCR) from the gastrointestinal tract. The encoding nucleic  
CC acid is useful for identifying or isolating chemical sensing receptors  
CC (including taste ion channels) and signaling molecules that would allow  
CC pharmacological and genetic modulation of taste transduction pathways.  
CC The native STC-1 enteroendocrine cells that naturally express GT2R are  
CC useful in identifying modulators of taste receptor-mediated signal  
CC transduction. These cells are also used as models for studying taste-  
CC mediated signal transduction  
XX  
SQ Sequence 309 AA;  
Query Match 100.0%; Score 1597; DB 6; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.2e-152;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MITPLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
DB 1 MITPLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
QY 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFSNWLATLISIFYLLKIANFSNFIPLH 120  
DB 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFSNWLATLISIFYLLKIANFSNFIPLH 120  
QY 121 LKRRVKSIVLVMLLGPLEFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
DB 121 LKRRVKSIVLVMLLGPLEFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
QY 181 MVANLVPFTLLTLLSFMLLICSCLKHLKQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
DB 181 MVANLVPFTLLTLLSFMLLICSCLKHLKQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFILSVFWMRYW 300  
DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFILSVFWMRYW 300  
QY 301 VKGEKTSSP 309  
DB 301 VKGEKTSSP 309  
RESULT 5  
ADC87039  
ID ADC87039 standard; protein; 309 AA.  
XX  
AC ADC87039;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human GPCR protein SEQ ID NO:1492.  
XX  
KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1270724-A2.  
XX  
PD 02-JAN-2003.

```

XX 18-JUN-2002; 2002EP-00013517.
XX PF
XX 18-JUN-2001; 2001JP-00246789.
XX PD
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
XX DR N-PSDB; ADC87038.
XX PT New polynucleotide, useful for preparing a composition for treating a
XX patient in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor.
XX PS Claim 2; SEQ ID NO 1492; 28pp; English.
XX CC The invention relates to a novel polynucleotide encoding a guanosine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX the invention may have a use in gene therapy. The polynucleotide and
XX polypeptide are useful for preparing a composition for treating a patient
XX in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor. The protein
XX sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX SQ Sequence 309 AA;
    Query Match      100.0%; Score 1597; DB 7; Length 309;
    Best Local Similarity 100.0%; Pred. No. 2.2e-152;
    Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKRQKISFADQILTALAVSRVGLLW 60
DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKRQKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLSIFYLLKIANFSNFIPLH 120
DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLSIFYLLKIANFSNFIPLH 120
QY 121 LKRRVKSIVLVMLLGPLLFLACHLFVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVMLLGPLLFLACHLFVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240
DB 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWSFGSLNKPVMFCKAIRFSYPSIHPFILLINGNKKLKQTFLSVFWQMRYW 300
DB 241 YFLSIMISVWSFGSLNKPVMFCKAIRFSYPSIHPFILLINGNKKLKQTFLSVFWQMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309
RESULT 6
ID ADR29240
AD ADR29240 standard; protein; 309 AA.
XX ADR29240;
XX AC ADR29240;
XX 04-NOV-2004 (first entry)
XX Taste receptor modulation-related human T2R61 protein sequence SeqID179.
XX T1R; T2R; taste receptor; G protein; modulatory compound; MAPK activity;
XX CAMP accumulation; adenylyl cyclase; bitter; taste; umami; sweet; T2R61;
XX human.
XX OS Homo sapiens.

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XX WO2004069191-A2.
XX PN
XX 19-AUG-2004.
XX PD
XX 03-FEB-2004; 2004WO-US002987.
XX PF
XX 03-FEB-2003; 2003US-0444172P.
XX PR 26-MAR-2003; 2003US-0457318P.
XX (SENO-) SENOMYX INC.
XX PA
XX Servant G, Ozeck M, Brust P, Xu H;
XX WPI; 2004-604341/58.
XX DR N-PSDB; ADR29239.
XX PT Identifying a compound that modulates the activity of a T1R or T2R taste
XX receptor by assaying the effect of the putative modulatory compound on
XX MAPK activation, cAMP accumulation or adenylyl cyclase activity in the
XX eukaryotic cell.
XX PS Disclosure; SEQ ID NO 179; 248pp; English.
XX CC This invention is related to a novel method of identifying a compound
XX that modulates the activity of a T1R or T2R taste receptor. The method
XX comprises providing a eukaryotic cell that expresses a functional T1R or
XX T2R taste receptor and a G protein that couples to it, contacting the
XX eukaryotic cell with a compound and identifying whether the compound
XX modulates the activity of T1R or T2R expressed by the eukaryotic cell
XX based on its effect on MAPK activity, cAMP accumulation or adenylyl
XX cyclase activity. The method is used to identify a compound that blocks
XX bitter taste associated with a particular T2R activator or that blocks or
XX enhances umami taste elicited by a compound that activates the T1R/T1R3
XX (umami) taste receptor or sweet taste elicited by a compound that
XX activates the T1R2/T1R3 (sweet) taste receptor. The method is useful in
XX identifying a compound that modulates the activity of a T1R or T2R taste
XX receptor. The present sequence is that of a human T2R taste receptor
XX protein which is related to the method of the invention.
XX SQ Sequence 309 AA;
    Query Match      100.0%; Score 1597; DB 8; Length 309;
    Best Local Similarity 100.0%; Pred. No. 2.2e-152;
    Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKRQKISFADQILTALAVSRVGLLW 60
DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKRQKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLSIFYLLKIANFSNFIPLH 120
DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLSIFYLLKIANFSNFIPLH 120
QY 121 LKRRVKSIVLVMLLGPLLFLACHLFVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVMLLGPLLFLACHLFVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240
DB 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWSFGSLNKPVMFCKAIRFSYPSIHPFILLINGNKKLKQTFLSVFWQMRYW 300
DB 241 YFLSIMISVWSFGSLNKPVMFCKAIRFSYPSIHPFILLINGNKKLKQTFLSVFWQMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309
RESULT 7
ADM33295

```

ID ADM33295 standard; protein; 309 AA.  
AC ADM33295;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human bitter taste receptor TAS2R43 protein SEQ ID NO:9.  
XX  
KW human; bitter taste receptor; food.  
XX  
OS Homo sapiens.  
XX  
PN WQ2004029087-A2.  
XX  
XX  
XX 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-EP010691.  
XX  
XX 25-SEP-2002; 2002US-0413298P.  
XX  
XX (DEER-) DEUT INST ERNAERUNGSFORSCHUNG POTSDAM.  
XX  
XX Bufo B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;  
XX WPI; 2004-305149/28.  
XX N-PSDB; ADM33296.  
XX  
XX Novel bitter receptor polynucleotide encoding human TAS2R protein having  
XX bitter substance binding activity, useful for producing nutraceutical or  
XX pharmaceutical compositions comprising antagonists of bitter taste  
XX receptor activity.  
XX  
XX Claim 1; SEQ ID NO 9; 108pp; English.  
XX  
XX The present sequence represents a human bitter taste receptor. Also  
XX described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)  
XX a vector (II) containing (I); (3) a host cell (III) genetically  
XX engineered with (I) or (II); (4) a transgenic non-human animal (IV)  
XX containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino  
XX acid sequence encoded by (I) or obtained by culturing (III) and  
XX recovering polypeptide; (6) an antibody (VI) specifically binding to (V);  
XX (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an  
XX antagonist/inhibitor (VIII) against (V) which is antibody, the  
XX extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
XX isolating (M1) a compound that binds to (V) encoded by (I); (10)  
XX isolating (M2) an antagonist of bitter taste receptor activity; (11) a  
XX foodstuff including human and animal foodstuff, any precursor material or  
XX additive employed in the production of foodstuff comprising (VIII); and  
XX (12) a nutraceutical/pharmaceutical composition comprising (VIII) and an  
XX active agent and optionally a carrier. (III) is useful for producing a  
XX polypeptide encoded by (I), which involves culturing (III) and recovering  
XX the polypeptide encoded by (I). (II) is useful for producing cells  
XX capable of expressing at least one of the bitter taste receptor  
XX polypeptide, which involves genetically cells in vitro with (II), where  
XX the bitter taste receptor polypeptide(s) is/are encoded by (I). (M1) or  
XX (M2) can be used for producing food or any precursor material or additive  
XX employed in the production of foodstuffs. (M1) or (M2) can also be used  
XX for producing nutraceutical or pharmaceutical compositions. (I), (II),  
XX (VI) or (VIII) can be used for manufacturing a medicament for the  
XX treatment of an abnormally increased or decreased sensitivity towards a  
XX bitter substance. The identified agonist/inhibitor efficiently suppresses  
XX or eliminated bitter tasting components of food and effectively useful in  
XX food industries.  
XX  
XX Sequence 309 AA;  
SQ  
Query Match 98.6%; Score 1575; DB 8; Length 309;  
Best Local Similarity 99.4%; Pred. No. 3.7e-150;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MITTELPITSSLVVTVFVIGNFANGFIALVNSIEFKQKISFADQILTALAVSRVGLLW 60  
DB 1 MITTELPITSSLVVTVFVIGNFANGFIALVNSIEFKQKISFADQILTALAVSRVGLLW 60

QY 61 VLLNNWYSTVLNPAFNSVEVTRTAYNIWAVINHFNSWNLATLTSIFYLLKIANFSNFIPLH 120  
DB 61 VLLNNWYSTVLNPAFNSVEVTRTAYNIWAVINHFNSWNLATLTSIFYLLKIANFSNFIPLH 120  
QY 121 LKRRVKSIVLNLGFLFLFLACHLFFVINNNEIVRTKBEFEGNMTWKIKLSAMYFSNMTVT 180  
DB 121 LKRRVKSIVLNLGFLFLFLACHLFFVINNNEIVRTKBEFEGNMTWKIKLSAMYFSNMTVT 180  
QY 181 MVANLVPPFTLLSPMLLICSCKHLKQMLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
DB 181 MVANLVPPFTLLSPMLLICSCKHLKQMLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLWGNKKLKOTFLSVFWMQRYW 300  
DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLWGNKKLKOTFLSVFWMQRYW 300  
QY 301 VKGKTSSTP 309  
DB 301 VKGKTSSTP 309  
RESULT 8  
ADM74420  
ID ADM74420 standard; protein; 309 AA.  
XX  
AC ADM74420;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Human bitter taste receptor protein T2R43 with an encoded SNP Seq 32.  
XX  
KW receptor; SNP detection; SAP; single amino acid polymorphism; screening;  
XX DNA microarray; flavor enhancer.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Misc-difference 35  
XX /label= Trp, Ser  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 90  
XX /label= Val  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 154  
XX /label= Arg, Gly  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 170  
XX /label= Ser, Arg  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 200  
XX /label= Cys, Phe  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 212  
XX /label= Arg, His  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 221  
XX /label= Thr  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 294  
XX /label= Phe, Leu  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 295  
XX /label= Trp, Arg  
XX /note= "Encoded by a single nucleotide polymorphism"  
XX Misc-difference 297  
XX /label= Met, Val  
XX /note= "Encoded by a single nucleotide polymorphism"  
PN WQ2005007891-A2.  
XX  
XX 27-JAN-2005.  
XX

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PF 18-JUN-2004; 2004WO-US019489.
XX
XX
PR 19-JUN-2003; 2003US-0480035P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Drayna D, Kim U;
XX
DR WPI; 2005-152091/16.
DR N-PSDB; ADW74419.
XX
XX
PT New isolated bitter taste receptor (T2R) variant-specific nucleic acid
PT molecule comprises at least 10 contiguous nucleotides, useful for
PT defining large groups of populations who perceive bitter tastes
PT differently.
XX
XX
XX Claim 18; SEQ ID NO 32; 567pp; English.
XX
XX This invention relates to novel human bitter taste receptor (T2R) variant
XX -specific nucleic acid molecules, each spanning at least one SNP
XX identified in the specification. Specifically, it refers to the T2R
XX allele nucleic acid molecules and the encoded proteins thereof. The
XX present invention describes a method of screening compounds useful for
XX modulating bitter taste and using a specific binding agent that is
XX capable of discriminating between two or more polypeptides. Accordingly,
XX it provides a method of determining the T2R genotype of a subject using
XX at least one oligonucleotide from each T2R haplotype/allele on a
XX microarray to identify T2R single nucleotide polymorphisms. As such, the
XX isolated T2R variant-specific nucleic acid molecules are useful in the
XX development of flavorings and flavor enhancers as it can be used to
XX define large groups of populations who perceive bitter tastes
XX differently. It is also used to identify compounds that interact
XX differently with different variants of a taste receptor. This polypeptide
XX sequence is a bitter taste receptor T2R protein of the invention.
XX
SQ Sequence 309 AA;
Query Match 95.1%; Score 1518; DB 9; Length 309;
Best Local Similarity 96.8%; Pred. No. 2.1e-144; Mismatches 10; Indels 0; Gaps 0;
Matches 299; Conservative 0;
QY 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFNSNWLATLTSIFYLLKIANFNFIFLH 120
DB 61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFNSNWLATLTSIFYLLKIANFNFIFLH 120
QY 121 LKRRVKSVLVNLGPGLLFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSVLVNLGPGLLFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPPFTLLTSFMLLICSCKHLKKQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
DB 181 MVANLVPPFTLLTSFMLLIXSLCKHLKKQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWSFGSLENKPVMPCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300
DB 241 YFLSIMISVWSFGSLENKPVMPCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309
RESULT 9
ID AAU11390
XX AAU11390 standard; protein; 309 AA.
XX AC AAU11390;
XX
DT 26-MAR-2002 (first entry)

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XX Human T2R75 (hT2R75) polypeptide.
XX
XX Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor;
XX hT2R75; T2R75; T2R; bitter taste sensation; taste signalling pathway;
XX taste transduction; food taste masking; drug taste masking.
XX
XX Homo sapiens.
XX
XX WO200177676-A1.
XX
XX 18-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US010739.
XX
XX 07-APR-2000; 2000US-0195532P.
XX 13-NOV-2000; 2000US-0247014P.
XX
XX (SENO-) SENOMYX INC.
XX
XX Adler JE;
XX
XX WPI; 2002-017486/02.
XX N-PSDB; AAS18173.
XX
XX Novel isolated mammalian taste cell-specific G protein-coupled receptor,
XX T2R, involved in bitter taste sensation, useful for identifying taste
XX modulators that are used to decrease or mask bitter taste of foods or
XX drugs.
XX
XX Claim 60; Page 75; 103pp; English.
XX
XX The invention relates to a mammalian taste cell-specific G protein-
XX coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste
XX sensation. The T2R polypeptides and their associated polynucleotides are
XX useful for screening one or more compounds for the presence of taste
XX detectable by a mammal. Modulators of T2R polypeptides (modulators of
XX taste transduction) are useful for pharmacological and genetic
XX modulations of taste signalling pathways. These modulatory compounds are
XX then used in food and pharmaceutical industries to customise taste, e.g.,
XX to decrease or mask the bitter taste of foods or drugs. This sequence
XX represents the human T2R75 (hT2R75) polypeptide
XX
SQ Sequence 309 AA;
Query Match 90.2%; Score 1440; DB 5; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.5e-136;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;
QY 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFNSNWLATLTSIFYLLKIANFNFIFLH 120
DB 61 VLLLNWYSTVLNPAFNSIEVRITAYNVWAVINHFNSNWLATLTSIFYLLKIANFNFIFLH 120
QY 121 LKRRVKSVLVNLGPGLLFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSVLVNLGPGLLFLACHLFVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPPFTLLTSFMLLICSCKHLKKQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
DB 181 ILANLVPPFTLLTSFLLICSCKHLKKQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWSFGSLENKPVMPCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300
DB 241 YFLSIMISVWSFESLENKPVMPCEAIFSYPSHPFILIWGNKKLKQTFLSVLMHVRW 300
QY 301 VKGEKTS 308
DB 301 VKGEKPSS 308

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RESULT 10  
 ABR58039  
 ID ABR58039 standard; protein; 309 AA.  
 XX  
 AC ABR58039;  
 XX  
 DT 25-JUL-2003 (first entry)  
 XX  
 DE Human GI endocrine cell specific GPCR GT2R-h54.  
 XX  
 KW Chemosensor; G-protein coupled receptor; GPCR; receptor; ion channel;  
 KW gastrointestinal tract; taste; enteroendocrine cell.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003031604-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 11-OCT-2002; 2002WO-US032664.  
 XX  
 PR 12-OCT-2001; 2001US-0328993P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (PHLE/) PHLEGER C S W.  
 XX  
 FI Walsh JH, Rozengurt JE, Wu SV;  
 XX  
 DR WPI; 2003-381713/36.  
 DR N-PSDB; ACC44475.  
 XX  
 PT New nucleic acid encoding a chemosensing G-protein coupled receptor,  
 PT useful for identifying chemical sensing receptors and signaling molecules  
 PT that allow pharmacological and genetic modulation of taste transduction  
 PT pathways.  
 XX  
 PS Disclosure; Page 92-93; 101pp; English.  
 XX  
 CC This sequence represents a novel isolated chemosensing G-protein coupled  
 CC receptor (GPCR) from the gastrointestinal tract. The encoding nucleic  
 CC acid is useful for identifying or isolating chemical sensing receptors  
 CC (including taste ion channels) and signaling molecules that would allow  
 CC pharmacological and genetic modulation of taste transduction pathways.  
 CC The native STC-1 enteroendocrine cells that naturally express GPCR are  
 CC useful in identifying modulators of taste receptor-mediated signal  
 CC transduction. These cells are also used as models for studying taste-  
 CC mediated signal transduction  
 XX  
 SQ Sequence 309 AA;  
 Query Match 90.2%; Score 1440; DB 6; Length 309;  
 Best Local Similarity 88.3%; Pred. No. 1.5e-136;  
 Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;  
 Qy 1 MITFLPIIFSSLVVVTFTVGNFANGFTALVNSIEWFKROKISFADQILTALAVSRVGLLW 60  
 Db 1 MITFLPIIFSSLVVVTFTVGNFANGFTALVNSIEWFKROKISFADQILTALAVSRVGLLW 60  
 Qy 61 VLLNNWYSTVLNPAFNSVEVRTTAYNIWAVINHFNSNWLATLTSIFYLLKIANFSNFIHL 120  
 Db 61 VLVLNWTATELNPAFNSIEVRITAYNVAVINHFNSNWLATLTSIFYLLKIANFSNFIHL 120  
 Qy 121 LKRRVKSIVLLMGLPFLFLACHLFPVINNNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180  
 Db 121 LKRRVKSIVLLMGLPFLFLACHLFPVINNNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180  
 Qy 181 MVANLVPTFTLLSFMILLICSLCKHKKMQLHGKSGQDPSKVIKALQTVISFLLLCAL 240  
 Db 181 ILANLVPTFTLLSFMILLICSLCKHKKMQLHGKSGQDPSKVIKALQTVISFLLLCAL 240  
 Qy 241 YFLSIMITSVNSFSGLENKPVMEFCKAIRFSYPSIHPFLLIWNKKLKQTFLSVFWQRYW 300  
 Db 241 YFLSIMITSVNSFSGLENKPVMEFCKAIRFSYPSIHPFLLIWNKKLKQTFLSVFWQRYW 300

RESULT 10  
 ABR58039  
 ID ABR58039 standard; protein; 309 AA.  
 XX  
 AC ABR58039;  
 XX  
 DT 25-JUL-2003 (first entry)  
 XX  
 DE Human GI endocrine cell specific GPCR GT2R-h54.  
 XX  
 KW Chemosensor; G-protein coupled receptor; GPCR; receptor; ion channel;  
 KW gastrointestinal tract; taste; enteroendocrine cell.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003031604-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 11-OCT-2002; 2002WO-US032664.  
 XX  
 PR 12-OCT-2001; 2001US-0328993P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (PHLE/) PHLEGER C S W.  
 XX  
 FI Walsh JH, Rozengurt JE, Wu SV;  
 XX  
 DR WPI; 2003-381713/36.  
 DR N-PSDB; ACC44475.  
 XX  
 PT New nucleic acid encoding a chemosensing G-protein coupled receptor,  
 PT useful for identifying chemical sensing receptors and signaling molecules  
 PT that allow pharmacological and genetic modulation of taste transduction  
 PT pathways.  
 XX  
 PS Disclosure; Page 92-93; 101pp; English.  
 XX  
 CC This sequence represents a novel isolated chemosensing G-protein coupled  
 CC receptor (GPCR) from the gastrointestinal tract. The encoding nucleic  
 CC acid is useful for identifying or isolating chemical sensing receptors  
 CC (including taste ion channels) and signaling molecules that would allow  
 CC pharmacological and genetic modulation of taste transduction pathways.  
 CC The native STC-1 enteroendocrine cells that naturally express GR2R are  
 CC useful in identifying modulators of taste receptor-mediated signal  
 CC transduction. These cells are also used as models for studying taste-  
 CC mediated signal transduction  
 XX  
 SQ Sequence 309 AA;  
 Query Match 90.2%; Score 1440; DB 6; Length 309;  
 Best Local Similarity 88.3%; Pred. No. 1.5e-136;  
 Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;  
 Qy 1 MITFLPIIFSSLVVVTFTVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60  
 Db 1 MITFLPIIFSSLVVVTFTVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60  
 Qy 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFNSNWLATTLSIFYLLKIANFSNFIHL 120  
 Db 61 VLVLNWTATELNPAFNSIEVRITAYNVAVINHFNSNWLATSLSIFYLLKIANFSNFIHL 120  
 Qy 121 LKRRVKSIVLMLLGPLLFLACHLFVINNMNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180  
 Db 121 LKRRVKSIVLMLLGPLLFLACHLFVINNMNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180  
 Qy 181 MVANLVPTLTLSFMILLICSLCKHKKMQLHGKSGQDPSKVIKALQTVISFLLLCAL 240  
 Db 181 ILANLVPTLTLSFMILLICSLCKHKKMQLHGKSGQDPSKVIKALQTVISFLLLCAL 240  
 Qy 241 YFLSIMITSVNSFSGLENKPVMEFCKAIRFSYPSIHPFLLIWNKKLKQTFLSVFWQRYW 300





CC differently. It is also used to identify compounds that interact  
CC differently with different variants of a taste receptor. This polypeptide  
CC sequence is a bitter taste receptor T2R haplotype protein that contains  
CC single amino acid polymorphisms encoded by DNA that features SNPs of the  
CC invention.

XX Sequence 309 AA;

SQ Query Match 90.2%; Score 1440; DB 9; Length 309;

Best Local Similarity 88.3%; Pred. No. 1.5e-136;

Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSILVVTFFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

Db 1 MITFLPIIFSSILVVTFFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLISIFVLLKIANFSNFIPLH 120

Db 61 VLVLNWYATELNPAFNSIEVRITAYNVAVINHFSNWLATLISIFVLLKIANFSNLIPLH 120

QY 121 LKRRVKSIVLVMGLPGLFLACHLFVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

Db 121 LKRRVKSIVLVMGLPGLFLACHLFVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

Db 181 ILANLVPFTLTLLSFMLLICSCLKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

QY 241 YFLSIMISVWSPGSLNKPVMFCKAIRFSYPSIHPFILLIWNKGLKQTFLSVFWQMRVW 300

Db 241 YFLSIIMSVMSPESLENKPVFMFCEAIAFSYPSHPFILLIWNKGLKQTFLSVFWQMRVW 300

QY 301 VKGEKTSS 308

Db 301 VKGEKPSS 308

RESULT 14

ADW74594

ID ADW74594 standard; protein; 309 AA.

XX AC ADW74594;

XX DT 07-APR-2005 (first entry)

XX DE Human bitter taste receptor haplotype protein T2R46 Seq 206.

XX KW receptor; SNP detection; SAP; single amino acid polymorphism; screening;

XX KW DNA microarray; flavor enhancer.

XX OS Homo sapiens.

XX PN WO2005007891-A2.

XX XX 27-JAN-2005.

XX PF 18-JUN-2004; 2004WO-US019489.

XX PR 19-JUN-2003; 2003US-0480035P.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Drayna D, Kim U;

XX DR WPI; 2005-152091/16.

XX DR N-PSDB; ADW74593.

XX PT New isolated bitter taste receptor (T2R) variant-specific nucleic acid

PT molecule comprises at least 10 contiguous nucleotides, useful for

PT defining large groups of populations who perceive bitter tastes

PT differently.

XX Claim 18; SEQ ID NO 206; 567pp; English.

XX This invention relates to novel human bitter taste receptor (T2R) variant  
CC -specific nucleic acid molecules, each spanning at least one SNP  
CC identified in the specification. Specifically, it refers to the T2R  
CC allele nucleic acid molecules and the encoded proteins thereof. The  
CC present invention describes a method of screening compounds useful for  
CC modulating bitter taste and using a specific binding agent that is  
CC capable of discriminating between two or more polypeptides. Accordingly,  
CC it provides a method of determining the T2R genotype of a subject using  
CC at least one oligonucleotide from each T2R haplotype/allele on a  
CC microarray to identify T2R single nucleotide polymorphisms. As such, the  
CC isolated T2R variant-specific nucleic acid molecules are useful in the  
CC development of flavorings and flavor enhancers as it can be used to  
CC define large groups of populations who perceive bitter tastes  
CC differently. It is also used to identify compounds that interact  
CC differently with different variants of a taste receptor. This polypeptide  
CC sequence is a bitter taste receptor T2R haplotype protein that contains  
CC single amino acid polymorphisms encoded by DNA that features SNPs of the  
CC invention.

XX Sequence 309 AA;

SQ Query Match 90.0%; Score 1438; DB 9; Length 309;

Best Local Similarity 88.0%; Pred. No. 2.4e-136;

Matches 271; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSILVVTFFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

Db 1 MITFLPIIFSSILVVTFFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLISIFVLLKIANFSNFIPLH 120

Db 61 VLVLNWYATELNPAFNSIEVRITAYNVAVINHFSNWLATLISIFVLLKIANFSNLIPLH 120

QY 121 LKRRVKSIVLVMGLPGLFLACHLFVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

Db 121 LKRRVKSIVLVMGLPGLFLACHLFVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

Db 181 ILANLVPFTLTLLSFMLLICSCLKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

QY 241 YFLSIMISVWSPGSLNKPVMFCKAIRFSYPSIHPFILLIWNKGLKQTFLSVFWQMRVW 300

Db 241 YFLSIIMSVMSPESLENKPVFMFCEAIAFSYPSHPFILLIWNKGLKQTFLSVFWQMRVW 300

QY 301 VKGEKTSS 308

Db 301 VKGEKPSS 308

RESULT 15

ADW74576

ID ADW74576 standard; protein; 309 AA.

XX AC ADW74576;

XX DT 07-APR-2005 (first entry)

XX DE Human bitter taste receptor haplotype protein T2R44 Seq 188.

XX KW receptor; SNP detection; SAP; single amino acid polymorphism; screening;

XX KW DNA microarray; flavor enhancer.

XX OS Homo sapiens.

XX PN WO2005007891-A2.

XX XX 27-JAN-2005.

XX PF 18-JUN-2004; 2004WO-US019489.

XX PR 19-JUN-2003; 2003US-0480035P.



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:16:01 ; Search time 42 Seconds  
(without alignments)  
707.880 Million cell updates/sec

Title: US-09-825-882-8  
Perfect score: 1597  
Sequence: 1 MITPLPIIFSSLVVTVFVIG.....FLSVFWMQRYVWVGKTSSTSP 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130.5	8.2	341	2 T26920	hypothetical prote
2	130.5	8.2	380	2 I38435	angiotensin recept
3	126.5	7.9	387	2 H82889	conserved hypothet
4	123	7.7	360	2 A57160	chemokine (C-C) re
5	120.5	7.5	441	2 A70346	conserved hypothet
6	117	7.3	360	2 JC4587	chemokine (C-C) re
7	116.5	7.3	316	2 S69659	hypothetical prote
8	115.5	7.2	363	2 JC2543	angiotensin II rec
9	115	7.2	311	2 A57223	pheromone receptor
10	115	7.2	358	2 T11165	ubiquinol-cytochro
11	114.5	7.2	825	2 T27852	hypothetical prote
12	112.5	7.0	312	2 A46750	olfactory receptor
13	112	7.0	355	2 T32241	hypothetical prote
14	112	7.0	1888	2 T33009	hypothetical prote
15	111.5	7.0	363	2 I48261	angiotensin II rec
16	111.5	7.0	505	2 B88206	protein F21D12.3 (
17	111	7.0	349	2 T23638	hypothetical prote
18	110.5	6.9	339	2 T25630	hypothetical prote
19	110.5	6.9	363	2 A49092	angiotensin II rec
20	110.5	6.9	386	2 T11286	ubiquinol-cytochro
21	110.5	6.9	538	1 D64164	hypothetical prote
22	109	6.8	432	2 H75622	integral membrane
23	108.5	6.8	387	2 S55550	5-Hr4S receptor -
24	108.5	6.8	406	2 S55549	serotonin 4 recept
25	108.5	6.8	770	2 G72589	hypothetical prote
26	108	6.8	380	2 JC2434	kappa opioid recep
27	107.5	6.7	317	2 T33861	hypothetical prote
28	107.5	6.7	336	2 T25180	hypothetical prote
29	106.5	6.7	268	2 T16851	hypothetical prote

RESULT 1

T26920

hypothetical protein Y45F10B.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Dec-2004

C:Accession: T26920

R:McMurray, A.

submitted to the EMBL Data Library, January 1998

A:Reference number: Z20286

A:Accession: T26920

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-341 <WIL>

A:Cross-references: UNIPROT:O62472; UNIPARC:UPI00000612B9; EMBL:AL021487; PIDN:CAAL16358

A:Experimental source: clone Y45F10B

C:Genetics:

A:Gene: CESP:Y45F10B.6

A:Map position: 4

A:Introns: 77/3; 147/3; 283/3

Query Match

Best Local Similarity 8.2%; Score 130.5; DB 2; Length 341;

Matches 71; Conservative 53; Mismatches 86; Indels 111; Gaps 20;

QY 1 MITPLPIIFSSLVVTVFVIGNFANGFIALVNSIEW---FKRQKISFADQILTALAVSRVG 57

Db LVATFPPIIY--LVPTVFIIFK-----VFKVFGSLFEKRMESLNPHVFLVIVVSQLT 77

QY 58 LLWVLLLMWYSTVLNPAFNSVEVRTAYNIWAVI---NHFSNWLATTLISIFYLLKI-ANP 113

Db SI-LYMISDYLITRIPF-----TGAITSWCAIQPNHF-----LKILFSLSIYFTF 122

QY 114 SNFIF-----LHLKRVKSV-----ILV-----MLL 134

Db TSWLFPSSLTLRVISYFPQQRKLSARISKAIPIYVYVFPFISFSLPALGFCRQLL 182

QY 135 GPLLFLACHLFINNNEIVRTKEFEGNMTWKILKLSAMYFGSNMTVTMVAN-----LVPF 188

Db GPYQFGAIYIW-----FSGN--W-----MEVYFTKIVLNIELNPFQIKIVGVF 224

QY 189 TLTLSFMLLTCSLC-----KHLKMQQLHGKS--QDPSTKVHKALQTVISFL--LLCA 239

Db VLNMI-FWLILCTLLNLFYRKLLKMSNHGKSATLQRAEYSLTLTTFSMLLSYITNLACA 283

QY 240 IYF-----LSIMISVMSFGS 254

Db LMFIFPSMLVYFIALRPFNG 304

RESULT 2

T38435

angiotensin receptor homolog APJ - human



Db 147 RARTLTGYVITSLATWSAVFASLP-----GFLFSTC--YTERNHYYCKTKY 191  
Qy 158 FEGNWTWKKLSAMVFSNMVTVMANLVPPFTLLSFMLLCSL--CKHLKMKQLHGKG 215  
Db 192 SLNSTYTKV-----LSLENIILGLVPIGIMLFCVSMIIRTLOHCKNEKN----- 238  
Qy 216 SODPSTKVHIKALQTVISPLLC-----AIYFLSIMISVMSFGSLENKPVFMFC--- 264  
Db 239 -----KAVKMFVAVVLFLGFWTPYNIIVLPLETLVEL-----EVLQDCTFE 279  
Qy 265 -----KAIRSYPSIHFPILLWGNKKLKQTFLSVF 294  
Db 280 RYLDVAIOATETLAFVHCCNLIPIYFFLGKPKRYILOLF 319

RESULT 5  
A70346  
conserved hypothetical protein aq\_509 - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: A70346  
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oviatt, D.; et al.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: A70346  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-441 <AQF>  
A:Cross-references: UNIPROT:O66797; UNIPARC:UPI0000056398; GB:AE000693; NID:g2983148; PIR:Q06797  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: aq\_509

Query Match 7.5%; Score 120.5; DB 2; Length 441;  
Best Local Similarity 22.2%; Pred. No. 0.027;  
Matches 76; Conservative 55; Mismatches 134; Indels 77; Gaps 16;  
Qy 7 IIPSSLVVTVFVIGNFANGFTALVNSIEWFKRQKISFADQILTALAVSRVGLLVLLNW 66  
Db 105 LLFTPTLLTGLTGLAIGFVPLVKI-----PVGFNNEALSYTQVAYFLLLPYLLPNF 158  
Qy 67 YSTVLNPAFNSVEVRTTAYNIWAVINHF-----SNMLATLSIFYLKIANF 113  
Db 159 LFPHFAGVLRVR-RFTYVFGFPLFSFPLFLGLFLFYKWLVLPLSISPAQIATL 217  
Qy 114 SNFI-----FLH-----LKRKSVILVMLLGLPFLFLACHLFINNNEIVRTKEFGNMTWK 165  
Db 218 YMFYVGRFHIINFPNQTTRKIINHFYLSALYGVHLF-----IVIDRAF-GSLIGE 270  
Qy 166 IKLSAMVFSNMVTVMANLVPPFTLLSFMLLCSLCK-HLKQMLHGKSGQDPSTKVH 224  
Db 271 -KSISAIHYG-----LIVASIPRGIRLENIAITLSSESGDKIKLNF-----Y 313  
Qy 225 IKALQTVISPLLCALYFLSISVMS-VMSFGSLENKPVFMFCALRFSYPSIHPFTLWIG- 282  
Db 314 IKRLIVSGISLAPFPFAEIIIVKLLFGYGAFTQMDLITVETATRF-YLSLPLFMFLMPI 372  
Qy 283 -----NKKLKQTF-----LSVFW--QMRYVWVG 303  
Db 373 LYRVFQIKENLKPVFIAISGITVNGILNYPFVLKLNYGIGK 414

RESULT 6  
JC4587  
chemokine (C-C) receptor 4 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: JC4587  
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to  
A:Reference number: JC4587; MUID:96136324; PMID:8573157  
A:Accession: JC4587  
A:Molecule type: mRNA  
A:Residues: 1-360 <HO>  
A:Cross-references: UNIPROT:P51680; UNIPARC:UPI0000028F3B; EMBL:X90862; NID:g1167851; PIR:Q05168  
A:Experimental source: thymus  
C:Genetics:  
A:Gene: cc ckr-4  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
F:72,483,194/Binding site: carboxydrate (Asn) (covalent) #status predicted  
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 7.3%; Score 117; DB 2; Length 360;  
Best Local Similarity 22.0%; Pred. No. 0.042;  
Matches 51; Conservative 44; Mismatches 75; Indels 62; Gaps 10;  
Qy 4 FLPIFSSLVVTVFVIGNFANGFTALVNSIEWFKRQKISFADQILTALAVS----- 54  
Db 41 FLPLPLYS-----LVFLLGLFGNSVVVLV--LPKYKELK-SMTDVLNLAISDLLFLVLSLP 93  
Qy 55 -----RVGELL-----WVLLNMYSTVLNPAFNSVEVRTTAYNIWAVINHFNSWL 98  
Db 94 FWGYVAAQDWVFLGLCKIVSMVYLVGYSGIFFIMLSID-----RYLAIVHAVFSLK 147  
Qy 99 ATTLSIFVLKIANFSNFIHLKRRKSVILVMLLGLPFLFLACHLFINNNEIVRTKEF 158  
Db 148 ARTLTGYVITSLTWSAVFASLP-----GLLFSTC--YTEHNHYCKTKQYS 192  
Qy 159 EGNMTWKKLSAMVFSNMVTVMANLVPPFTLLSFMLLCSL--CKHLK 208  
Db 193 VNSTWKV-----LSLEINVLGLLPIGLIMLFYWSMIIRTLOHCKNEK 237

RESULT 7  
S69659  
hypothetical protein YDR492w - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C>Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 31-Dec-2004  
C:Accession: S69659; S69664  
R:Dieckrich, F.S.  
submitted to the EMBL Data Library, August 1995  
A:Description: The sequence of S. cerevisiae coemids 9410, 8035, 8166, and 9787.  
A:Reference number: S69554  
A:Accession: S69659  
A:Molecule type: DNA  
A:Residues: 1-316 <DIE>  
A:Cross-references: UNIPROT:Q03419; UNIPARC:UPI000006B9A1; EMBL:U33050; NID:g927726; PIR:Q03419  
C:Genetics:  
A:Gene: MIPS:YDR492w  
A:Map position: 4R  
C:Superfamily: Adiponectin receptor protein and homologs

Query Match 7.3%; Score 116.5; DB 2; Length 316;  
Best Local Similarity 21.1%; Pred. No. 0.04;  
Matches 45; Conservative 39; Mismatches 66; Indels 63; Gaps 8;  
Qy 150 NEIVRTKEFGNMTWKIKLSAMVFSNMVTVMANLVPPFTLLSFMFL-----FTLLSFMFL----- 197  
Db 53 NDKILTGVVRETLGKCKLYSLFYNNETVNIYTHLVPAIVYFVFAITLTNYFLIPVPPS 112  
Qy 198 -----LICSCLKHLKQMLHGKSGQDPSTKVHIKALQTVISPLLC 238  
Db 113 TWSDDYTVINIFLMGAFSCLMCSFCFC--MKQHSKQSNFWSKLDYLGIIISLSCSMP 170  
Qy 239 AIYV-LSIMISVMSFGSLENKPVFMFCAL-----RFSYPSIHP-----FILLWG----- 282  
Db 171 IYFGYFDHISYFLSFTVITVLATFTCTVCLVHDKFNTSTPRPRAMPFFILFGSGLLPL 230  
Qy 283 -----NKKLKQTFLSVFMQRYVWVG 303



A;Gene: CESP:ZK418.6  
A;Introns: 24/3; 53/3; 98/2; 153/1; 196/3; 269/1; 338/2; 394/2; 444/1; 562/2; 6

Query Match 7.2%; Score 114.5; DB 2; Length 825;  
Best Local Similarity 19.6%; Pred. No. 0.15;  
Matches 68; Conservative 60; Mismatches 116; Indels 103; Gaps 14;

Qy 4 FLPIPSSVVVTVFVIGNFANGFIALVNSIEWPKRQKISPADQILTALAVSR-----V 56  
Db :  
65 FLAIIPMVLGIITFIIN--LGY--LIAIKCFRYETMGFKKR--EAFLLMRSSSNIFAI 117  
Qy :  
57 GLLVLLLNWYSIVLN-----PAFNSEVEVTAYNIWAVINHFSNWLATT 101  
Db :  
118 VLFYVILVWKVNGFNYSAMIFIIGGSTFMSTGIYIVLTIVILYNVAHHISYMTTIT 177  
Qy :  
102 LS-----IFYLLKIANFSNFIFLHL-----KRRVKSVILVML---- 133  
Db :  
178 LTHCWLIIGLIWIISTVTSVFVGWGATLFYPDSAPFTCSFESCOQLAIVIMLSICY 237  
Qy 134 ---LGPLLFLACHLFINNMNEIVRTKEFGNMTWKILKLSAMYFSNTVTM---VANLVP 187  
Db :  
238 GTVIG--LYIA--MMARIHQLR-----KSMVOARCNNSMIAMRRLLSNNMIT 282  
Qy 188 FTLTLLSFMLLICSLCHKHAKMQHLHGKSODPSTKVHIKALQTWISPLLLCAIVFLSIMI 247  
Db :  
283 FAIGTDPIILVICIVALVNKLSELGSGCKSPCKTFR-----LSYLLIDVENMASISA 335  
Qy 248 SVMSFGSLENKPVMFCFAIRFSYPSHPFILGWGNKKLKQTFLSVF 294  
Db :  
336 IVMLIAMAD-----PVNILSDKLAGVRIKQF 364

RESULT 12  
A46750  
Olfactory receptor homolog - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A46750  
R;Abbe, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S.  
J. Biol. Chem. 268, 12033-12039, 1993  
A;Title: Primary structure and cell-type specific expression of a gustatory G P  
A;Note: sequence extracted from NCBI backbone (NCBIN:133352, NCBI:P:133353)  
C;Superfamily: olfactory receptor OR14  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 7.0%; Score 112.5; DB 2; Length 312;  
Best Local Similarity 19.9%; Pred. No. 0.083;  
Matches 63; Conservative 63; Mismatches 120; Indels 71; Gaps 14;

Qy 8 IFSSLVVTVFVIGNFANGFIALVNS-----IEWFKRKISFADQILTALAVSRVGLLW 61  
Db :  
11 LFLSWILVT-VLGNLL--IILAESSHLNLMYFFLSNLSFVDICISTTIPTK----- 61

Qy 62 LLNLNWSTVLNPAFNSEVEVTAYNIWAVINHFSNWLATTLSITYLLKIANSFNP-IFLH 120  
Db :  
62 MLNVHSQTKDISV--IECLSQVYFL--TFEGGMDFILLTMACDRYVAICHPLNYTYVMN 118

Qy 121 LKRVKSVILVMLGPLLFLACHLFINNMNEI-----VRTKEGNTWKIKL-KSAMYF 174  
Db :  
119 LQ----LCALLITLMFLWMFCVSIIHLLNMELNFSRGTEIPHFPCELAQVLKVAUSDTHI 175

Qy 175 SNM---TVTMVANIVPFTLLSFLMLLICSLCHKHAKMQHLHGKSODPSTKVHIKALQTV 231  
Db :  
176 NNPFMVYTSELGLIPWTGILMYSQIASLLMKSSSVSKY-----KAPESTC 222

Qy 232 ISFLLLCAIYFLSIMITSVWSFGSLENKPVMFCFAIRFS-----YPSIHFP 277



```

Db      223 GSHLCVSVLFYGSATL-----VYFCSSVLHSTHKKMIASLWYTVTISPMLNPF 269
QY      278 ILIWNKKLQKTFLSV 294
Db      270 IYSLRNKDVKGALGKLF 286

RESULT 13
T32241
hypothetical protein T15B7.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32241
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T15B7.
A:Reference number: Z21139
A:Accession: T32241
A:Status: Preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-355 <PAU>
A:Cross-references: UNIPROT:O17029; UNIPARC:UPI000007FF98; EMBL:AF022985; PIDN:AAB69970.
A:Experimental source: strain Bristol N2; clone T15B7
C:Gene: CESP-T15B7.11
A:Gene position: 5
A:Map position: 36/2; 103/2; 150/2; 185/2; 219/3; 255/2; 295/2

Query Match      7.0%; Score 112; DB 2; Length 355;
Best Local Similarity 24.7%; Pred. No. 0.1;
Matches 74; Conservative 48; Mismatches 88; Indels 90; Gaps 16;

QY      8  IFSSLVVTTCGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVGL-----LWVLL 63
Db      45  LLSSLIVFSF-----FANILIVIVLS---HKEMRHSGINIVIMFIADVDFGCVAVTGLMOLF 97
QY      64  LNWYSTVLNPAFNSVEVRTAY-----NIWAVINHFNS-WLATTLSIFVLKIANFSNFI 117
Db      98  IRNYS-----DQWMLFTAYLQFVDYLVAVFHASLFLAAGWALCRVMAL-NFSN-- 147
QY      118 FHLKRRKRS---VILVMLLGPLLFLACHLFVINNEIVRTKEFE-----GNM 162
Db      148  ---RLDKWGSRYALRVTCVAVITVLTSLVPVNEVKTTDDGEVIDTSDFLAYGCL 205
QY      163 TWKIKLKSAFYNSNTVTWVANLVPTLTLLSFMLLICSLCHKLKKMQLHGKSGQDPSTX 222
Db      206 LMKIVL-----VFGICFPLPCTLMLLLSILL-----LQKMD-EGKRSSVPINR 249
QY      223 VHKK-----ALQTVISFLLLCAI-----YF--LSIMISVNSF 252
Db      250 NHHKRVQDLDRSSQLTIQILIVFLITEVPEQGVFSIGGIEVIDYLYNQNLTFIMNVLSP 309

RESULT 14
T39009
hypothetical protein SPAC6B12.02c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39009
R:Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z21815
A:Accession: T39009
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1888 <GEN>
A:Cross-references: UNIPROT:O14207; UNIPARC:UPI000013AA2F; EMBL:Z98531; PIDN:CAB11064.1;
A:Experimental source: strain 972h-; cosmid c6B12
C:Gene: SPDB:SPAC6B12.02c
A:Gene position: 1
C:Superfamily: Schizosaccharomyces hypothetical protein SPAC6B12.02c
```

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Query Match      7.0%; Score 112; DB 2; Length 1888;
Best Local Similarity 19.2%; Pred. No. 0.56;
Matches 75; Conservative 59; Mismatches 128; Indels 128; Gaps 19;

QY      1  MITPLPIFFSLVVV---TFVIGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVG 57
Db      801  LVEKIAVLVQTFQVVFYCEFELGNQN-----INKVSLA-----SDLISKLLSAGQSG 849
QY      58  LLWVLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFNSWMLATTLSIFYLKIANFSNP- 116
Db      850  ----LLECYRNLRIOASDITVIDTFLFLESNLIH-----LFHYVKKYKLYALWEQVN 897
QY      117  IFLHLKRRVKSVI-----LVMLLGPLLFLACHLFVINNEIVRTKEFEGNMT-WKIKL 168
Db      898  SFFDLQKKELSIEMEKIYVIMTLNP-----VFQIGLN---GTTSHSPGNNSFWPLII 947
QY      169  KSA-----MYFSNMVTVTWVANLVPTLTLLSFM-----LICSCLKHLKKMQ 210
Db      948  RVSESAFQKHKGDNVKKVVERYLRTVFLRIHFLISEWEDVAQILFLIDFFFSHRKEND 1007
QY      211  LHGKSGQDPST-----KVHIKALQTVISFLLLCATYFLSMTI----- 247
Db      1008  LSSEISIEDPTDFDFVKSLDRPPNHLVLTALDT-----CFVIYLVKILISISLRQVD 1060
QY      248  -----SVWSPGSLKPKVPMFC---KAIRFSYPSIHPF 277
Db      1061  ENTNSIKRIVSRLOPLHSRQVTRSPFSIKDFMSLEHTHLICLYWAAPENCPSLNRI 1120
QY      278  --ILIWNKKLQKTFLSV-FW--QMRVWK 302
Db      1121  RDIVVDNSHLKARLISLKAMLHLMKYVIK 1150

RESULT 15
T48261
angiotensin II receptor type 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: T48261; JC2028
R:Horiuchi, M.; Koike, G.; Yamada, T.; Mukoyama, M.; Nakajima, M.; Dzau, V.J.
J. Biol. Chem. 270, 20225-20230, 1995
A:Title: The growth-dependent expression of angiotensin II type 2 receptor is regulated
A:Reference number: T48261; MUID:95378283; PMID:7650042
A:Accession: T48261
A:Status: translation not shown; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-363 <RES>
A:Cross-references: UNIPROT:P35374; UNIPARC:UPI000000185D; EMBL:U11073; NID:g607834; PID
B:Nakajima, M.; Mukoyama, M.; Pratt, R.E.; Horiuchi, M.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 197, 393-399, 1993
A:Title: Cloning of cDNA and analysis of the gene for mouse angiotensin II type 2 recept
A:Reference number: JC2028; MUID:94092107; PMID:8267573
A:Accession: T48261
A:Molecule type: mRNA
A:Residues: 1-363 <NAK>
A:Cross-references: UNIPARC:UPI000000185D; GB:U04828; NID:g439862; PIDN:AAC52128.1; PID:
C:Comment: This protein is the biologically active peptide of the renin-angiotensin syst
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:46-71/Domain: transmembrane #status predicted <TM1>
F:81-102/Domain: transmembrane #status predicted <TM2>
F:120-140/Domain: transmembrane #status predicted <TM3>
F:161-179/Domain: transmembrane #status predicted <TM4>
F:209-234/Domain: transmembrane #status predicted <TM5>
F:257-278/Domain: transmembrane #status predicted <TM6>
F:286-313/Domain: transmembrane #status predicted <TM7>
F:4.13,24,29,34/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:79,152,348,353/Binding site: phosphate (Ser) (covalent) #status predicted
F:346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match      7.0%; Score 111.5; DB 2; Length 363;
Best Local Similarity 20.7%; Pred. No. 0.12;
```



```
Matches 69; Conservative 65; Mismatches 132; Indels 67; Gaps 17;
Qy 5 LPIIFSSLVVTVFVIGNFANGFIAL-----VNSIEWFKRQKISFADQIILTALAV 53
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
47 IPVLY-----YMIFVIG-PAVNIVVWSLFCQKQPKVSSIYIF---NLALADLLLLATLP 98
Qy 54 SRVGLLWVLLNW-YSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLSIFYL--LXI 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
99 -----LMATYYSRYDMLFGP-----VMCKVFGSFLTLNMPA-----SIFFITCM SV 140
Qy 111 ANFSNFIPLHLKRRVKS-----VILVMLLGPLLFLACHLFVINMNEIVRTKEFEENMTW 164
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141 DRYQSVIYFPLSQRRNPWQASVYVPLWCMACLSSLPTFP-----RDVRTIETILGVNAC 195
Qy 165 KIKLSAMYFS-NMTVTWVANLVPPFTLLSFMLLTCSLCKHLKQMLHGKG--SQDPST 221
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 IMAPPPEKYAQSAGIALMKNILGFIIPLIATCYFGIRKHLKKTNSYGKNRITRDQVL 255
Qy 222 KVHIKALQTVISFLLLCALYP--LSMISVWSFGSLENKPVFM-----FCKAIRFSYP 272
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 KM---AAAVVLAF-IICWLPFHVLTFLDALTWGIIINSCEVIAVIDLALPFAILLGFTNS 311
Qy 273 SIHPFILLWGNKKLQOTFLSVFMQRYVYVKGK 305
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
312 CVNPFYCFVGNRFQOKLRSVFRVPITWLQGR 344
```

Search completed: April 27, 2006, 21:19:35  
Job time : 43 secs

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2006, 21:13:26 ; Search time 166 Seconds  
(without alignments)  
1313.303 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MITFLPIFFSLVWVFVIG.....FLSVFMQRYVWVGKGTSP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1579	98.9	309	1 T2R43_PANTR	Q646b4 pan troglod
2	1578	98.8	309	1 T2R43_PANPA	Q5Y500 pan paniscu
3	1575	98.6	309	1 T2R43_HUMAN	P59537 homo sapien
4	1575	98.6	309	1 Q645X4_HUMAN	Q645x4 homo sapien
5	1489	93.2	290	2 Q5UG21_PANTR	Q5UG21 pan troglod
6	1463	91.6	285	2 Q50KJ2_HUMAN	Q50Kj2 homo sapien
7	1453	91.0	309	1 T2R44_PANPA	Q646e0 pan paniscu
8	1450	90.8	285	2 Q50KJ1_PANTR	Q50Kj1 pan troglod
9	1448	90.7	309	1 T2R44_PANTR	Q646b9 pan troglod
10	1440	90.2	309	1 T2R46_HUMAN	P59540 homo sapien
11	1427	89.4	309	1 T2R44_HUMAN	P59538 homo sapien
12	1427	89.4	309	1 T2R46_PANPA	Q646e1 pan paniscu
13	1419	88.9	309	1 T2R44_PONPY	Q645v3 pongo pygma
14	1418	88.8	309	1 T2R46_PANTR	Q646c0 pan troglod
15	1412	88.4	309	1 T2R46_GORGO	Q645z7 gorilla gor
16	1411	88.4	309	1 T2R45_PANPA	Q5Y4z8 pan paniscu
17	1405	88.0	309	1 T2R46_PANPA	Q5Y4y8 pan paniscu
18	1396	87.4	309	1 T2R44_GORGO	Q645z6 gorilla gor
19	1394	87.3	296	2 Q5UG24_PANTR	Q5UG24 pan troglod
20	1382	86.5	309	1 T2R44_PAPHA	Q646f9 papio hamad
21	1361.5	85.3	308	1 T2R43_PAPHA	Q646f8 papio hamad
22	1359.5	85.1	309	1 T2R43_MACMU	Q645t3 macaca mula
23	1335	83.6	299	1 T2R45_HUMAN	P59539 homo sapien
24	1335	83.6	299	2 Q50KH4_MACMU	Q50Kh4 macaca mula
25	1334	83.5	285	2 Q50KH0_HUMAN	Q50Kh0 homo sapien
26	1333	83.5	298	2 Q50KH5_MACMU	Q50Kh5 macaca mula
27	1332	83.4	285	2 Q50KH1_HUMAN	Q50Kh1 homo sapien
28	1318	82.5	319	2 Q50KH2_9PRIM	Q645z8 gorilla gor
29	1317	82.5	319	1 T2R47_PONPY	Q645v4 pongo pygma
30	1311	82.1	285	2 Q50KG8_PANTR	Q50Kg8 pan troglod
31	1309	82.0	319	1 T2R47_PANTR	Q646c1 pan troglod

32	1306	81.8	309	1 T2R46_PAPHA	Q646g0 papio hamad
33	1304	81.7	319	1 T2R47_PANPA	Q646e2 pan paniscu
34	1295	81.1	272	2 Q50KI4_HYLAG	Q50Ki4 hylobates a
35	1293	81.0	319	1 T2R47_HUMAN	P59541 homo sapien
36	1292.5	80.9	308	1 T2R46_MACMU	Q645t4 macaca mula
37	1292	80.9	285	2 Q50KG9_PANTR	Q50Kg9 pan troglod
38	1291	80.8	285	2 Q50KI1_PANTR	Q50Ki1 pan troglod
39	1290	80.8	285	2 Q50KI7_TRACR	Q50Ki7 trachypithe
40	1286	80.5	285	2 Q50KI0_9PRIM	Q50Ki0 gorilla gor
41	1283.5	80.4	285	2 Q5XU77_MACMU	Q5Xu77 macaca mula
42	1278	80.0	285	2 Q50KI2_HUMAN	Q50Ki2 homo sapien
43	1273	79.7	285	2 Q50KI9_MACMU	Q50Ki9 macaca mula
44	1272	79.6	285	2 Q50KJ0_MACMU	Q50Kj0 macaca mula
45	1270	79.5	296	2 Q50KG4_PONPY	Q50Kg4 pongo pygma

#### ALIGNMENTS

#### RESULT 1

ID	T2R43_PANTR	STANDARD;	PRT;	309 AA.
AC	Q646B4;			
DT	01-FEB-2005 (Rel. 46, Created)			
DT	01-FEB-2005 (Rel. 46, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Taste receptor type 2 member 43 (T2R43).			
GN	Name=TAS2R43;			
OS	Pan troglodytes (Chimpanzee).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Pan.			
OX	NCBI_TaxID=9598;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	PubMed:15496349; DOI=10.1093/molbev/msi027;			
RA	Fischer A., Gildad Y., Man O., Paabo S.;			
RT	"Evolution of bitter taste receptors in humans and apes.";			
RL	Mol. Biol. Evol. 22:432-436(2005).			
CC	- - FUNCTION: Receptor that may play a role in the perception of bitterness and is gustducin-linked. May play a role in sensing the chemical composition of the gastrointestinal content. The activity of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 activation and lead to the gating of TRPM5 (By similarity).			
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- - MISCELLANEOUS: Most taste cells may be activated by a limited number of bitter compounds; individual taste cells can discriminate among bitter stimuli.			
CC	- - SIMILARITY: Belongs to the G-protein coupled receptor T2R family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	-----			
CC	EMBL; AY724889; AAU21105.1; -; Genomic_DNA.			
CC	InterPro; IPR007960; TAS2_recept.			
CC	PANTHER; PTHR11394; TAS2_recept; 1.			
CC	Pfam; PF05296; TAS2R; 1.			
CC	G-protein coupled receptor; Glycoprotein; Receptor;			
CC	Sensory transduction; Taste; Extracellular (Potential).			
CC	TOPO_DOM 1 1			
CC	TOPO_DOM 2 22			
CC	TOPO_DOM 23 46			
CC	TOPO_DOM 47 67			
CC	TOPO_DOM 68 86			
CC	TOPO_DOM 87 107			
CC	TOPO_DOM 108 126			
CC	TOPO_DOM 127 147			
CC	TOPO_DOM 148 178			
CC	TOPO_DOM 179 199			
CC	TOPO_DOM 200 229			

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FT TRANSMEM 230 250 6 (Potential).
FT TOPO DOM 251 259 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 176 176 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 309 AA; 35612 MW; 504332C099242D52 CRC64;

Query Match 98.9%; Score 1579; DB 1; Length 309;
Best Local Similarity 98.4%; Pred. No. 9.9e-108;
Matches 304; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
Db 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
Db 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
QY 121 LKRRVKSUILVMLLGPFLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSUILVMLLGPFLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPFTLLTSLFMLLICSCKHLKQMLHKGSGDPSTKVHIKALQTVISFLLCAI 240
Db 181 MVANLVPFTLLTSLFMLLICSCKHLKQMLHKGSGDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWFGSLNKPVMFCFAIRFSPYSIHPFILIWGNKKLKQTFILSVFQWRYW 300
Db 241 YFLSIMISVWFGSLNKPVMFCFAIRFSPYSIHPFILIWGNKKLKQTFILSVFQWRYW 300
QY 301 VKGEKTSPP 309
Db 301 VKGEKTSPP 309

RESULT 2
T2R43 PANPA STANDARD; PRT; 309 AA.
AC Q5Y500;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Taste receptor type 2 member 43 (T2R43).
GN Name=TAS2R43;
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9597;
RN [1]
RX NUCLEOTIDE SEQUENCE.
PubMed=15466715; DOI=10.1073/pnas.0404894101;
RA Parry C.M., Erkner A., le Coutre J.;
RT "Divergence of T2R chemosensory receptor families in humans, bonobos,
RT and chimpanzees";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14830-14834 (2004).
CC -!- FUNCTION: Receptor that may play a role in the perception of
CC bitterness and is gustducin-linked. May play a role in sensing the
CC chemical composition of the gastrointestinal content. The activity
CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC activation and lead to the gating of TRPM5 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
CC discriminate among bitter stimuli.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC EMBL; AY677147; AAV28575.1; -, Genomic_DNA.
DR InterPro; IPR007960; TAS2_recept.
DR PANTHER; PTHR11394; TAS2_recept; 1.
DR Pfam; PF05296; TAS2R; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor;
KW Sensory transduction; Taste; Transducer; Transmembrane.
FT TOPO DOM 1 1 Extracellular (Potential).
FT TRANSMEM 2 22 1 (Potential).
FT TOPO DOM 23 46 Cytoplasmic (Potential).
FT TRANSMEM 47 67 2 (Potential).
FT TOPO DOM 68 86 Extracellular (Potential).
FT TRANSMEM 87 107 3 (Potential).
FT TOPO DOM 108 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT TOPO DOM 148 178 Extracellular (Potential).
FT TRANSMEM 179 199 5 (Potential).
FT TOPO DOM 200 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT TOPO DOM 251 259 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 176 176 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 309 AA; 35611 MW; A4F4DPE412C4DD99 CRC64;

Query Match 98.8%; Score 1578; DB 1; Length 309;
Best Local Similarity 98.4%; Pred. No. 1.2e-107;
Matches 304; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
Db 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
Db 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
QY 121 LKRRVKSUILVMLLGPFLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSUILVMLLGPFLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPFTLLTSLFMLLICSCKHLKQMLHKGSGDPSTKVHIKALQTVISFLLCAI 240
Db 181 MVANLVPFTLLTSLFMLLICSCKHLKQMLHKGSGDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWFGSLNKPVMFCFAIRFSPYSIHPFILIWGNKKLKQTFILSVFQWRYW 300
Db 241 YFLSIMISVWFGSLNKPVMFCFAIRFSPYSIHPFILIWGNKKLKQTFILSVFQWRYW 300
QY 301 VKGEKTSPP 309
Db 301 VKGEKTSPP 309

RESULT 3
T2R43 HUMAN STANDARD; PRT; 309 AA.
ID T2R43_HUMAN
AC P59537; P59546;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Taste receptor type 2 member 43 (T2R43) (T2R52).
GN Name=TAS2R43;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RX NUCLEOTIDE SEQUENCE.
MEDLINE=22297730; PubMed=12379855; DOI=10.1038/ng1014;

```



Best Local Similarity 99.4%; Pred. No. 2e-107; Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MITPLPIFFSSLVVTVFVIGNPANGFIALVNSIEWFKRKISFADQILTALAVSRVGLW 60  
 DB 1 MITPLPIFFSSLVVTVFVIGNPANGFIALVNSIESFKRKISFADQILTALAVSRVGLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120  
 DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLVMGLPLFLACHLFLVINNEIVRTKEPEGNNMTWKIKLSAMYFSNMTVT 180  
 DB 121 LKRRVKSIVLVMGLPLFLACHLFLVINNEIVRTKEPEGNNMTWKIKLSAMYFSNMTVT 180

QY 181 MYANLVPPFTLLSPMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240  
 DB 181 MYANLVPPFTLLSPMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YFLSTMISVWSGSLNKPVMFCKAIRFSYPSIHPFILINGNKKLKQTFLSVFWQMY 300  
 DB 241 YFLSTMISVWSGSLNKPVMFCKAIRFSYPSIHPFILINGNKKLKQTFLSVFWQMY 300

QY 301 VKGKTSPP 309  
 DB 301 VKGKTSPP 309

RESULT 5  
 Q5UG21 PANTR PRELIMINARY; PRT; 290 AA.  
 AC Q5UG21 PANTR PRELIMINARY; PRT; 290 AA.  
 DT 01-FEB-2005 (TREMBLrel. 29, Created)  
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
 DE Candidate bitter taste receptor TAS2R43 (Fragment).  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 EX PubMed:15367488; DOI=10.1093/hmg/ddh289;  
 RA Wang X., Thomas S.D., Zhang J.;  
 RT "Relaxation of selective constraint and loss of function in the evolution of human bitter taste receptor genes."  
 RL Hum. Mol. Genet. 13:2671-2678(2004).  
 DR EMBL; AY736059; AAU47352.1; -; Genomic DNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR GO; GO:0005099; P:perception of taste; IEA.  
 DR InterPro; IPR007960; TAS2\_recept.  
 DR PANTHER; PTHR11394; TAS2\_Recept.  
 DR Pfam; PF05296; TAS2R; 1.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 290  
 SQ SEQUENCE 290 AA; 33390 MW; BB8D30AF746C46CC CRC64;

Query Match 93.2%; Score 1489; DB 2; Length 290;  
 Best Local Similarity 99.3%; Pred. No. 3.6e-101;  
 Matches 288; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 SSVLVVTVFVIGNPANGFIALVNSIEWFKRKISFADQILTALAVSRVGLWVLLNWTST 69  
 DB 1 SSVLVVTVFVIGNPANGFIALVNSIEWFKRKISFADQILTALAVSRVGLWVLLNWTST 60

QY 70 VLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSVI 129  
 DB 61 VLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSVI 120

QY 130 LVMLLGPFLFLACHLFLVINNEIVRTKEPEGNNMTWKIKLSAMYFSNMTVTWVANLVPP 189  
 DB 130 LVMLLGPFLFLACHLFLVINNEIVRTKEPEGNNMTWKIKLSAMYFSNMTVTWVANLVPP 180

QY 190 LTLSPMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFLSIMISV 249  
 DB 190 LTLSPMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFLSIMISV 240

QY 250 WSPGSLNKPVMFCKAIRFSYPSIHPFILINGNKKLKQTFLSVFWQMY 299  
 DB 250 WSPGSLNKPVMFCKAIRFSYPSIHPFILINGNKKLKQTFLSVFWQMY 290

RESULT 6  
 Q50KJ2 HUMAN PRELIMINARY; PRT; 285 AA.  
 AC Q50KJ2 HUMAN PRELIMINARY; PRT; 285 AA.  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Bitter taste receptor T2R43 (Fragment).  
 GN Name=Hosa (Biaka) -T2R43;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Go Y., Satta Y., Takahata N.;  
 RT "Lineage-Specific Loss of Function of Bitter Taste Receptor Genes in Humans and Nonhuman Primates."  
 RL Genetics 170:313-326(2005).  
 DR EMBL; AB199182; BAD98056.1; -; Genomic DNA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 285  
 SQ SEQUENCE 285 AA; 32657 MW; 36880236D179A620 CRC64;

Query Match 91.6%; Score 1463; DB 2; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-99;  
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FSSLVVTVFVIGNPANGFIALVNSIEWFKRKISFADQILTALAVSRVGLWVLLNWTST 68  
 DB 1 FSSLVVTVFVIGNPANGFIALVNSIEWFKRKISFADQILTALAVSRVGLWVLLNWTST 60

QY 69 TVLPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSV 128  
 DB 61 TVLPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSV 120

QY 129 ILVMLLGPFLFLACHLFLVINNEIVRTKEPEGNNMTWKIKLSAMYFSNMTVTWVANLVPP 188  
 DB 129 ILVMLLGPFLFLACHLFLVINNEIVRTKEPEGNNMTWKIKLSAMYFSNMTVTWVANLVPP 180

QY 189 TLTLSFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFLSIMIS 248  
 DB 181 TLTLSFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFLSIMIS 240

QY 249 WSPGSLNKPVMFCKAIRFSYPSIHPFILINGNKKLKQTFLSV 293  
 DB 241 WSPGSLNKPVMFCKAIRFSYPSIHPFILINGNKKLKQTFLSV 285

RESULT 7  
 T2R44 PANPA STANDARD; PRT; 309 AA.  
 ID T2R44 PANPA STANDARD; PRT; 309 AA.  
 AC Q646E0; Q51429;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)



DE Taste receptor type 2 member 44 (T2R44).  
GN Name=TA2R44;  
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Pan.  
OX NCBI\_TaxID=9597;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15466715; DOI=10.1093/molbev/msi027;  
RA Fischer A., Gilad Y., Man O., Paabo S.;  
RT "Evolution of bitter taste receptors in humans and apes.";  
RL Mol. Biol. Evol. 22:432-436(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15466715; DOI=10.1073/pnas.0404894101;  
RA Parry C.M., Erkner A., le Coutre J.;  
RT "Divergence of T2R chemosensory receptor families in humans, bonobos,  
and chimpanzees.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:14830-14834(2004).  
CC -!- FUNCTION: Receptor that may play a role in the perception of  
bitterness and is gustducin-linked. May play a role in sensing the  
chemical composition of the gastrointestinal content. The activity  
of this receptor may stimulate alpha gustducin, mediate PLC-beta-2  
activation and lead to the gating of TRPM5 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited  
number of bitter compounds; individual taste cells can  
discriminate among bitter stimuli.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
CC EMBL; AY724849; AAU21079.1; -; Genomic DNA.  
CC EMBL; AY677148; AAV28576.1; -; Genomic DNA.  
CC InterPro: IPR007960; TAS2\_recept.  
CC PANTHER: PTHR11394; TAS2\_recept.  
CC Pfam; PF05296; TAS2R; 1.  
CC G-protein coupled receptor; Glycoprotein; Receptor;  
CC Sensory transduction; Taste; Transducer; Transmembrane.  
FT TOPO\_DOM 1 2 Extracellular (Potential).  
FT TRANSMEM 3 23 1 (Potential).  
FT TOPO\_DOM 24 55 Cytoplasmic (Potential).  
FT TRANSMEM 56 76 2 (Potential).  
FT TOPO\_DOM 77 100 Extracellular (Potential).  
FT TRANSMEM 101 121 3 (Potential).  
FT TOPO\_DOM 122 126 Cytoplasmic (Potential).  
FT TRANSMEM 127 147 4 (Potential).  
FT TOPO\_DOM 148 181 Extracellular (Potential).  
FT TRANSMEM 182 202 5 (Potential).  
FT TOPO\_DOM 203 229 Cytoplasmic (Potential).  
FT TRANSMEM 230 250 6 (Potential).  
FT TOPO\_DOM 251 259 Extracellular (Potential).  
FT TRANSMEM 260 280 7 (Potential).  
FT TOPO\_DOM 281 309 Cytoplasmic (Potential).  
FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 5 5 L -> I (in Ref. 2).  
FT CONFLICT 116 116 F -> L (in Ref. 2).  
SQ SEQUENCE 309 AA; 35357 MW; 5E15295BBD59A7AA CRC64;  
Query Match 91.0%; Score 1453; DB 1; Length 309;  
Best Local Similarity 90.9%; Pred. No. 1.7e-98;  
Matches 281; Conservative 11; Mismatches 17; Indels 0; Gaps 0;  
QY 1 MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVGLLW 60  
Db 1 MTFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVGLLW 60  
QY 61 VLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLH 120

Db 61 VLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLH 120  
QY 121 LKRRVKSIVLLVMLGPKLLFLACHLPVINNMNEIVRTK3FEGNNTWKIKLKSAFYFSNMTVT 180  
Db 121 LKRRVKSIVLLVMLGPKLLFLACHLPVINNMNEIVRTK3FEGNNTWKIKLKSAFYFSNMTVT 180  
QY 181 MVANLVPEFTLLSFMLLICSCLCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
Db 181 TLGNLVPEFTLLCLFLLLICSCLCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240  
QY 241 YFLSIMISVWSFGSLEKNKPVFMFCKAIRFSPSIHPFILIWGNKKLKQTFILSVFQMRYW 300  
Db 241 YFLSIMISVWSFGSLEKNKPVFMFCKAIRFSPSIHPFILIWGNKKLKQTFILSVLRQVRW 300  
QY 301 VKGSKTSSP 309  
Db 301 VKGSKPSSP 309  
RESULT 8  
O50KJ1\_PANTR PRELIMINARY; PRT; 285 AA.  
AC O50KJ1;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Bitter taste receptor T2R43 (Fragment).  
GN Name=Patr-T2R43;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Go Y., Satta Y., Takenaka O., Takahata N.;  
RT "Lineage-Specific Loss of Function of Bitter Taste Receptor Genes in  
Humans and Nonhuman Primates.";  
RL Genetics 170:313-326(2005).  
DR EMBL; AB199183; BAD98057.1; -; Genomic DNA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
FT NON\_TER 1 1  
FT NON\_TER 285 285  
SQ SEQUENCE 285 AA; 32597 MW; 40EF9BDDC6418FF4 CRC64;  
Query Match 90.8%; Score 1450; DB 2; Length 285;  
Best Local Similarity 98.6%; Pred. No. 2.6e-98;  
Matches 281; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 9 FSSLVVTVFVIGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVGLLWLLLNWYS 68  
Db 1 FSSLVVTVFVIGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVGLLWLLLNWYS 60  
QY 69 TVLNPAFNSVEVTTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLHKKRVKSV 128  
Db 61 TVLNPAFNSVEVTTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLHKKRVKSV 120  
QY 129 ILVNLGPKLLFLACHLPVINNMNEIVRTK3FEGNNTWKIKLKSAFYFSNMTVTWVANLVPP 188  
Db 121 ILVNLGPKLLFLACHLPVINNMNEIVRTK3FEGNNTWKIKLKSAFYFSNMTVTWVANLVPP 180  
QY 189 TLTLLSFMLLICSCLCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLLCALYFISIMIS 248  
Db 181 TLTLLSFMLLICSCLCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLLCALYFISIMIS 240  
QY 249 VWSFGSLEKNKPVFMFCKAIRFSPSIHPFILIWGNKKLKQTFILSV 293  
Db 241 VWSFGSLEKNKPVFMFCKAIRFSPSIHPFILIWGNKKLKQTFILSV 285  
RESULT 9



CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2  
CC activation and lead to the gating of TRPM5 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells  
CC of the tongue and exclusively in gustducin-positive cells.  
CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited  
CC number of bitter compounds; individual taste cells can  
CC discriminate among bitter stimuli.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC DR EMBL: AV114091; AAM63541.1; -; Genomic DNA.  
CC DR EMBL: AV724941; AU21143.1; -; Genomic DNA.  
CC DR EMBL: AF494227; AAM19318.1; -; Genomic DNA.  
CC DR Ensembl: ENSG00000184861; Homo sapiens.  
CC DR HGNC: HGNC:18877; TAS2R46.  
CC DR InterPro: IPR007960; TAS2\_recept.  
CC DR PANTHER: PTHR11394; TAS2\_recept; 1.  
CC DR Pfam: PF05296; TAS2R; 1.  
CC KW G-protein coupled receptor; Glycoprotein; Receptor;  
CC Sensory transduction; Taste; Transducer; Transmembrane.  
CC FT TOPO\_DOM 1 1 Extracellular (Potential).  
CC FT TRANSMEM 2 22 1 (Potential).  
CC FT TOPO\_DOM 23 46 Cytoplasmic (Potential).  
CC FT TRANSMEM 47 67 2 (Potential).  
CC FT TOPO\_DOM 68 86 Extracellular (Potential).  
CC FT TRANSMEM 87 107 3 (Potential).  
CC FT TOPO\_DOM 108 126 Cytoplasmic (Potential).  
CC FT TRANSMEM 127 147 4 (Potential).  
CC FT TOPO\_DOM 148 178 Extracellular (Potential).  
CC FT TRANSMEM 179 199 5 (Potential).  
CC FT TOPO\_DOM 200 229 Cytoplasmic (Potential).  
CC FT TRANSMEM 230 250 6 (Potential).  
CC FT TOPO\_DOM 251 259 Extracellular (Potential).  
CC FT TRANSMEM 260 280 7 (Potential).  
CC FT TOPO\_DOM 281 309 Cytoplasmic (Potential).  
CC FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).  
CC FT CONFLICT 228 228 L -> M (in Ref. 2).  
CC FT CONFLICT 296 297 HV -> QM (in Ref. 3).  
CC SQ SEQUENCE 309 AA; 35523 MW; FF4D7747F0CE47EF CRC64;  
Query Match 90.2%; Score 1440; DB 1; Length 309;  
Best Local Similarity 88.3%; Pred. No. 1.5e-97;  
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;  
QY 1 MITFLPIFSSLIWVTFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60  
DB 1 MITFLPIFSSLIWVTFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60  
QY 61 VLLLNWYSTLVNPAFNSVEVRTTAYNIWAVINHFNSNLATLTSIFYLLKIANFSNFIHL 120  
DB 61 VLVLNWYATFLNPAFNSIEVRITAYNVAVINHFNSNLATLSIFYLLKIANFSNFIHL 120  
QY 121 LKRRVKSVLVLMGLPLFLACHLFFVINNVEIVRKEFGNNTWKLSAMVFSNMTVT 180  
DB 121 LKRRVKSVLVLMGLPLFLACHLFFVINNVEIVRKEFGNNTWKLSAMVFSNMTVT 180  
QY 181 MVANLVPPFTLLSLFMLLCSLCKHLKQMLGKGSQDPSKVHKLQTVISFLLLCAL 240  
DB 181 IUANLVPPFTLLSLFLLLSLCKHLKQMLGKGSQDPSKMHVHKLQTVISFLLLCAL 240  
QY 241 YFLSIMISVMSGSLNKPVMFCIAIRFSYPSIHPFILLGNKKLQKTFLSVFMQRYW 300  
DB 241 YFLSIIMSVMFSLENNKVPVNFCEAIAFSYSTHPPFILLGNKKLQKTFLSVLMHVRW 300  
QY 301 VKGKTPSS 308  
|||||

Db 301 VKGKTPSS 308  
RESULT 11  
T2R44 HUMAN STANDARD; PRT; 309 AA.  
ID P59538; P59547; Q645X5;  
AC 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Taste receptor type 2 member 44 (T2R44) (T2R53).  
GN Name=TAS2R44; (Human).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22297730; PubMed=12379855; DOI=10.1159/000068546;  
RA Conte C., Ebbling M., Marcuz A., Nef P., Andres-Barquin P.J.;  
RT "Identification and characterization of human taste receptor genes  
belonging to the TAS2R family.";  
RL Cytogenet. Genome Res. 98:45-53 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15496549; DOI=10.1093/molbev/msi027;  
RA Fischer A., Gilad Y., Man O., Paabo S.;  
RT "Evolution of bitter taste receptors in humans and apes.";  
RL Mol. Biol. Evol. 22:432-436 (2005).  
RN [4]  
RP MEDLINE=22135574; PubMed=12139982; DOI=10.1016/S0959-4388(02)00345-8;  
RA Montmayeur J.-P., Matsunami H.;  
RT "Receptors for bitter and sweet taste.";  
RL Curr. Opin. Neurobiol. 12:366-371 (2002).  
RN [5]  
RP REVIEW.  
RX MEDLINE=21634924; PubMed=11696554; DOI=10.1074/jbc.R100054200;  
RA Margolskee R.F.;  
RT "Molecular mechanisms of bitter and sweet taste transduction.";  
RL J. Biol. Chem. 277:1-4 (2002).  
RN [6]  
RP REVIEW.  
RX MEDLINE=22469025; PubMed=12581520; DOI=10.1016/S0092-8674(03)00071-0;  
RA Zhang Y., Hoon M.A., Chandrasekar J., Mueller K.L., Cook B., Wu D.,  
Zucker C.S., Ryba N.J.;  
RT "Coding of sweet, bitter, and umami tastes: different receptor cells  
sharing similar signaling pathways.";  
RL Cell 112:293-301 (2003).  
RN [7]  
RP ACTIVATION BY SACHARIN AND ACESULFAME K.  
RX PubMed=15537898; DOI=10.1523/JNEUROSCI.1225-04.2004;  
RA Kuhn C., Bufo B., Winnig M., Hofmann T., Frank O., Behrens M.,  
Lewtschenko T., Slack J.P., Ward C.D., Meyerhof W.;  
RT "Bitter taste receptors for saccharin and acesulfame K.";  
RL J. Neurosci. 24:10260-10265 (2004).  
CC -!- FUNCTION: Receptor that may play a role in the perception of  
CC bitterness and is gustducin-linked. May play a role in sensing the  
CC chemical composition of the gastrointestinal content. The activity  
CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2  
CC activation and lead to the gating of TRPM5 (By similarity).  
CC Activated by the sulfonyl amide sweeteners saccharin and  
CC acesulfame K.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells

CC	of the tongue and exclusively in gustducin-positive cells.
CC	-1- MISCELLANEOUS: Most taste cells may be activated by a limited
CC	number of bitter compounds; individual taste cells can
CC	discriminate among bitter stimuli.
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	
DR	ENBL; AF494328; AAM19319.1; -; Genomic_DNA.
DR	ENBL; AY114090; AAM63540.1; -; Genomic_DNA.
DR	ENBL; AY724942; AAU21144.1; -; Genomic_DNA.
DR	Ensembl; ENSG00000183205; Homo sapiens.
DR	HGNC; HGNC:18881; TAS2R44.
DR	InterPro; IPR007960; TAS2_recept.
DR	PANTHER; PTHR11394; TAS2_recept; 1.
DR	Pfam; PF05296; TAS2R; 1.
KW	G-protein coupled receptor; Glycoprotein; Receptor;
KW	Sensory transduction; Taste; Transducer; Transmembrane.
FT	TOPO_DOM 1 23
FT	TRANSEM 3 23
FT	TOPO_DOM 24 55
FT	TRANSEM 56 76
FT	TOPO_DOM 77 100
FT	TRANSEM 101 121
FT	TOPO_DOM 122 126
FT	TRANSEM 127 147
FT	TOPO_DOM 148 181
FT	TRANSEM 182 202
FT	TOPO_DOM 203 229
FT	TRANSEM 230 250
FT	TOPO_DOM 251 259
FT	TRANSEM 260 280
FT	TOPO_DOM 281 309
FT	CARBOHYD 161 161
FT	CONFLICT 162 162
FT	CONFLICT 227 227
FT	CONFLICT 240 240
FT	SEQUENCE 309 AA; 35296 MW; 56937C13952CB828 CRC64;
Query Match	89.4%; Score 1427; DB 1; Length 309;
Best Local Similarity	89.6%; Pred.No. 1.3e-96;
Matches 277; Conservative	12; Mismatches 20; Indels 0; Gaps 0;
Qy	1 MTFLPTIFSSLVVTVFVIGNFANGFTALVNSIERVKRQKISPADQILTALAVSRVGLLW 60
Db	:     :     :     :     :     :     :     :     :
Qy	61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFNSNLATTLISFYLLKIANFSNFIHL 120
Db	:     :     :     :     :     :     :     :
Qy	121 LKRVKSVILVMLGLPLLFLACHLFVINNMIEIVRTKEFEGNMWTKIKLKAIFYSNMTVT 180
Db	:     :     :     :     :     :     :     :
Qy	181 MVANLVPFTLTLSFMLLICSLCHKLKKMQLHGKSGODPSTKVHIKALQTVIFSLLLCAI 240
Db	:     :     :     :     :     :     :     :
Qy	241 YFLSIMISVMSFGSLENKPVFMFCKAIRFSYPSIHPIILWGNKKLKQTFSLVFMQRYW 300
Db	:     :     :     :     :     :     :     :
Qy	301 VKGEKTSPP 309
Db	:     :     :     :     :     :     :     :
Qy	301 VKGEKTSPP 309
Db	:     :     :     :     :     :     :     :

ID	T2R46_PANPA	STANDARD;	PRT;	309 AA.
AC	Q646E1; Q5Y4Z7;			
DT	01-FEB-2005 (Rel. 46, Created)			
DT	01-FEB-2005 (Rel. 46, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Taste receptor type 2 member 46 (T2R46).			
GN	Name=TAS2R46;			
OS	Pan paniscus (Pygmy chimpanzee) (Bonobo).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Pan.			
OX	NCBI_TaxID=9597;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RP	PubMed=15496549; DOI=10.1093/molbev/msi027;			
RA	Fischer A., Gilad Y., Man O., Paabo S.;			
RT	"Evolution of bitter taste receptors in humans and apes.;"			
RL	Mol. Biol. Evol. 22:432-436(2005).			
RL	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RP	PubMed=15466715; DOI=10.1073/pnas.0404894101;			
RA	Barry C.M., Erkner A., le Coutre J.;			
RT	"Divergence of T2R chemosensory receptor families in humans, bonobos,			
RT	and chimpanzees.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 101:14830-14834(2004).			
CC	-1- FUNCTION: Receptor that may play a role in the perception of			
CC	bitterness and is gustducin-linked. May play a role in sensing the			
CC	chemical composition of the gastrointestinal content. The activity			
CC	of this receptor may stimulate alpha gustducin, mediate PLC-beta-2			
CC	activation and lead to the gating of TRPM5 (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- MISCELLANEOUS: Most taste cells may be activated by a limited			
CC	number of bitter compounds; individual taste cells can			
CC	discriminate among bitter stimuli.			
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	EMBL; AY724848; AAU21078.1; -; Genomic DNA.			
DR	EMBL; AY677150; AAV28578.1; -; Genomic DNA.			
DR	InterPro: IPR007960; TAS2_recept.			
DR	PANTHER; PTHR11394; TAS2_Recept; 1.			
DR	Pfam; PF05296; TAS2R; 1.			
KW	G-protein coupled receptor; Glycoprotein; Receptor;			
KW	Sensory transduction; Taste; Transducer; Transmembrane.			
FT	TOPO_DOM 1 1			
FT	TRANSEM 2 22			
FT	TOPO_DOM 23 45			
FT	TRANSEM 47 67			
FT	TOPO_DOM 68 86			
FT	TRANSEM 87 107			
FT	TOPO_DOM 108 126			
FT	TRANSEM 127 147			
FT	TOPO_DOM 148 178			
FT	TRANSEM 179 199			
FT	TOPO_DOM 200 229			
FT	TRANSEM 230 250			
FT	TOPO_DOM 251 259			
FT	TRANSEM 260 280			
FT	TOPO_DOM 281 309			
FT	CARBOHYD 161 161			
FT	CARBOHYD 176 176			
FT	CONFLICT 177 177			
FT	CONFLICT 305 305			
FT	CONFLICT 309 309			
FT	SEQUENCE 309 AA; 35644 MW; D1CF5966165C2B73 CRC64;			
SQ				

Query Match 89.4%; Score 1427; DB 1; Length 309;

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Best Local Similarity 87.4%; Pred. No. 1.3e-96;
Matches 270; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
FT TOPO DOM 24 55 Cytoplasmic (Potential).
FT TRANSMEM 56 76 2 (Potential).
FT TOPO DOM 77 100 Extracellular (Potential).
FT TRANSMEM 101 121 3 (Potential).
FT TOPO DOM 122 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT TOPO DOM 148 181 Extracellular (Potential).
FT TRANSMEM 182 202 5 (Potential).
FT TOPO DOM 203 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT TOPO DOM 251 259 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 309 AA; 35338 MW; 2B7C5152D4A36810 CRC64;

Query Match 88.9%; Score 1419; DB 1; Length 309;
Best Local Similarity 88.7%; Pred. No. 5.2e-96;
Matches 274; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
Db 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60

QY 61 VLLNWSYTVLNPAPNSVEVETAYNIWAVINHFNSNLATLSIPYLLKIANFSNFIPLH 120
Db 61 ALLNWSYTVENPAFYSVGVRTTVVDTVWTVGHFSNWLATSLSIPYLLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLWMLGPLLFLACHLVINNMNIRVTKFEGNMTWKIKLSAMYSNMTVT 180
Db 121 LKRRVKSIVLWMLGPLLFLACHLVINNMNIRVTKFEGNMTWKIKLSAMYSNMTVT 180

QY 181 MVANLVPPFTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240
Db 181 TLANLVPPFTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240

QY 241 YFLSIMISVMSFGSLENKPVFMFCARFSPSIHPFILIWGNKKLQTFILSVFQMRYW 300
Db 241 YFLSIMISVMSFGSLENKPVFMFCARFSPSIHPFILIWGNKKLQTFILSVLRQVRYW 300

QY 301 VKGEKTSPP 309
Db 301 VKGEKPSSP 309

RESULT 14
T2R44 PANTR
ID T2R44 PANTR STANDARD; PRT; 309 AA.
AC Q646C0;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Taste receptor type 2 member 46 (T2R46).
GN Name=TAS2R46;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OC NCBI_TaxID=9598;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15496549; DOI=10.1093/molbev/msi027;
RX Fischer A., Gilad Y., Man O., Paabo S.;
RA "Evolution of bitter taste receptors in humans and apes.";
RT Mol. Biol. Evol. 22:432-436(2005).
CC -1- FUNCTION: Receptor that may play a role in the perception of
CC bitterness and is gustducin-linked. May play a role in sensing the
CC chemical composition of the gastrointestinal content. The activity
CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC activation and lead to the gating of TRPM5 (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
CC discriminate among bitter stimuli.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY724974; AAU21166.1; -, Genomic_DNA.
CC InterPro; IPR007960; TAS2_recept.
CC DR PANTHER; PTHR11394; TAS2_recept.
CC DR Pfam; PF05296; TAS2R; 1.
CC KW G-protein coupled receptor; Glycoprotein; Receptor;
CC Sensory transduction; Taste; Transducer; Transmembrane.
CC FT TOPO_DOM 1 2 Extracellular (Potential).
CC TRANSMEM 3 23 1 (Potential).
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FT TOPO_DOM 24 55 Cytoplasmic (Potential).
FT TRANSMEM 56 76 2 (Potential).
FT TOPO_DOM 77 100 Extracellular (Potential).
FT TRANSMEM 101 121 3 (Potential).
FT TOPO_DOM 122 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT TOPO_DOM 148 181 Extracellular (Potential).
FT TRANSMEM 182 202 5 (Potential).
FT TOPO_DOM 203 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT TOPO_DOM 251 259 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO_DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 309 AA; 35338 MW; 2B7C5152D4A36810 CRC64;

Query Match 88.9%; Score 1419; DB 1; Length 309;
Best Local Similarity 88.7%; Pred. No. 5.2e-96;
Matches 274; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
Db 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60

QY 61 VLLNWSYTVLNPAPNSVEVETAYNIWAVINHFNSNLATLSIPYLLKIANFSNFIPLH 120
Db 61 ALLNWSYTVENPAFYSVGVRTTVVDTVWTVGHFSNWLATSLSIPYLLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLWMLGPLLFLACHLVINNMNIRVTKFEGNMTWKIKLSAMYSNMTVT 180
Db 121 LKRRVKSIVLWMLGPLLFLACHLVINNMNIRVTKFEGNMTWKIKLSAMYSNMTVT 180

QY 181 MVANLVPPFTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240
Db 181 TLANLVPPFTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240

QY 241 YFLSIMISVMSFGSLENKPVFMFCARFSPSIHPFILIWGNKKLQTFILSVFQMRYW 300
Db 241 YFLSIMISVMSFGSLENKPVFMFCARFSPSIHPFILIWGNKKLQTFILSVLRQVRYW 300

QY 301 VKGEKTSPP 309
Db 301 VKGEKPSSP 309

RESULT 14
T2R45 PANTR
ID T2R45 PANTR STANDARD; PRT; 309 AA.
AC Q646C0;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Taste receptor type 2 member 46 (T2R46).
GN Name=TAS2R46;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OC NCBI_TaxID=9598;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15496549; DOI=10.1093/molbev/msi027;
RX Fischer A., Gilad Y., Man O., Paabo S.;
RA "Evolution of bitter taste receptors in humans and apes.";
RT Mol. Biol. Evol. 22:432-436(2005).
CC -1- FUNCTION: Receptor that may play a role in the perception of
CC bitterness and is gustducin-linked. May play a role in sensing the
CC chemical composition of the gastrointestinal content. The activity
CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC activation and lead to the gating of TRPM5 (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
CC discriminate among bitter stimuli.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY724974; AAU21166.1; -, Genomic_DNA.
CC InterPro; IPR007960; TAS2_recept.
CC DR PANTHER; PTHR11394; TAS2_recept.
CC DR Pfam; PF05296; TAS2R; 1.
CC KW G-protein coupled receptor; Glycoprotein; Receptor;
CC Sensory transduction; Taste; Transducer; Transmembrane.
CC FT TOPO_DOM 1 2 Extracellular (Potential).
CC TRANSMEM 3 23 1 (Potential).
```

```

CC      discriminate among bitter stimuli.
CC      -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AY724877; AAU21099.1; -; Genomic_DNA.
CC      InterPro; IPR007960; TAS2_recept.
CC      PANTHER; PTHR11394; TAS2_recept; 1.
CC      Pfam; PF05296; TAS2R; 1.
CC      G-protein coupled receptor; Glycoprotein; Receptor;
CC      Sensory transduction; Taste; Transducer; Transmembrane.
CC      TOPO_DOM 1 1
CC      TRANSMEM 2 22
CC      TOPO_DOM 23 46
CC      TRANSMEM 47 67
CC      TOPO_DOM 68 86
CC      TRANSMEM 87 107
CC      TOPO_DOM 108 126
CC      TRANSMEM 127 147
CC      TOPO_DOM 148 178
CC      TRANSMEM 179 199
CC      TOPO_DOM 200 229
CC      TRANSMEM 230 250
CC      TOPO_DOM 251 259
CC      TRANSMEM 260 280
CC      TOPO_DOM 281 309
CC      TRANSMEM 309 AA; 35603 MW; 0AB71A246FC89322 CRC64;
CC      CARBOHYD 161 161
CC      N-linked (GlcNAc...) (Potential).
CC      SEQUENCE 309 AA; 35603 MW; 0AB71A246FC89322 CRC64;
CC      -----
Query Match      88.8%; Score 1418; DB 1; Length 309;
Best Local Similarity 87.1%; Pred. No. 6.1e-96;
Matches 269; Conservative 20; Mismatches 20; Indels 0; Gaps 0;
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DB      1 MITPLPIFFSLIIVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
QY      61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120
DB      61 VLLLNWYATELNPAPYSIEVRIITAYNWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120
QY      121 LKRRVKSIVLVMGLGPLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFNSMTVT 180
DB      121 LKRRVKSIVLVLGLGPLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFNSMTVT 180
QY      181 MVANLVPFTLTLLSFMLLICSCKHLKKWQLHGKSGQDPSTKVHKAQTIVTSFLLCAI 240
DB      181 ILANLVPFTLTLLSFMLLICSCKHLKKWQLHGKSGQDPSTKVHKAQTIVTSFLLCAI 240
QY      241 YFLSIMISVWSFGSLNKPVMFCKAIRFSPSIHPFLLINGNKKLKQTFLSVLHVRVW 300
DB      301 VKGEKTSPP 309
DB      301 VKGEKSPXP 309
RESULT 15
T2R46 GORGO
ID T2R46 GORGO STANDARD; PRT; 309 AA.
AC Q64527;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Taste receptor type 2 member 46 (T2R46).
GN Name=TAS2R46;
OS Gorilla gorilla gorilla (Lowland gorilla).

```

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Gorilla.
OX      NCBI_TaxID=9595;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=15496549; DOI=10.1093/molbev/msi027;
RA      Fischer A., Gilad Y., Man O., Paabo S.;
RT      "Evolution of bitter taste receptors in humans and apes.";
RL      Mol. Biol. Evol. 22:432-436(2005).
CC      -!- FUNCTION: Receptor that may play a role in the perception of
CC      bitterness and is gustducin-linked. May play a role in sensing the
CC      chemical composition of the gastrointestinal content. The activity
CC      of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC      activation and lead to the gating of TRPM5 (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- MISCELLANEOUS: Most taste cells may be activated by a limited
CC      number of bitter compounds; individual taste cells can
CC      discriminate among bitter stimuli.
CC      -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AY724911; AAU21122.1; -; Genomic_DNA.
CC      InterPro; IPR007960; TAS2_recept.
CC      PANTHER; PTHR11394; TAS2_recept; 1.
CC      Pfam; PF05296; TAS2R; 1.
CC      G-protein coupled receptor; Glycoprotein; Receptor;
CC      Sensory transduction; Taste; Transducer; Transmembrane.
CC      TOPO_DOM 1 1
CC      TRANSMEM 2 22
CC      TOPO_DOM 23 46
CC      TRANSMEM 47 67
CC      TOPO_DOM 68 86
CC      TRANSMEM 87 107
CC      TOPO_DOM 108 126
CC      TRANSMEM 127 147
CC      TOPO_DOM 148 178
CC      TRANSMEM 179 199
CC      TOPO_DOM 200 229
CC      TRANSMEM 230 250
CC      TOPO_DOM 251 259
CC      TRANSMEM 260 280
CC      TOPO_DOM 281 309
CC      TRANSMEM 309 AA; 35567 MW; 886893EDP27FF521 CRC64;
CC      CARBOHYD 161 161
CC      N-linked (GlcNAc...) (Potential).
CC      SEQUENCE 309 AA; 35567 MW; 886893EDP27FF521 CRC64;
CC      -----
Query Match      88.4%; Score 1412; DB 1; Length 309;
Best Local Similarity 86.7%; Pred. No. 1.7e-95;
Matches 267; Conservative 22; Mismatches 19; Indels 0; Gaps 0;
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DB      1 MITPLPIFFSLIIVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
QY      61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120
DB      61 VLLLNWYATELNPAPYSIEVRIITAYNWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120
QY      121 LKRRVKSIVLVMGLGPLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFNSMTVT 180
DB      121 LKRRVKSIVLVLGLGPLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFNSMTVT 180
QY      181 MVANLVPFTLTLLSFMLLICSCKHLKKWQLHGKSGQDPSTKVHKAQTIVTSFLLCAI 240
DB      181 ILANLVPFTLTLLSFMLLICSCKHLKKWQLHGKSGQDPSTKVHKAQTIVTSFLLCAI 240
QY      241 YFLSIMISVWSFGSLNKPVMFCKAIRFSPSIHPFLLINGNKKLKQTFLSVFMQRYW 300
DB      241 YFLSIMISVWSFGSLNKPVMFCKAIRFSPSIHPFLLINGNKKLKQTFLSVFMQRYW 300

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Db 241 YFLSVMSVWSFBSLENKPVFMFCEAITFSYPSTHPPFILWGNKCLKQTFLSVLWHVRYW 300  
Qy 301 VKGEKTSS 308  
|||  
Db 301 VKGEKPSS 308

Search completed: April 27, 2006, 21:18:41  
Job time : 167 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2006, 21:16:11 ; Search time 47 Seconds  
(without alignments)  
543.549 Million cell updates/sec

Title: US-09-825-882-8  
Perfect score: 1597  
Sequence: 1 MITFLPIIFSSLVVVFVIG.....FLSVFWMQRYVWVGKTSPP 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgm2\_6/ptodata/1/1aa/5 COMB.pep.\*  
2: /cgm2\_6/ptodata/1/1aa/6 COMB.pep.\*  
3: /cgm2\_6/ptodata/1/1aa/H COMB.pep.\*  
4: /cgm2\_6/ptodata/1/1aa/pCtus COMB.pep.\*  
5: /cgm2\_6/ptodata/1/1aa/RE COMB.pep.\*  
6: /cgm2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1115.5	69.8	300	2	US-09-393-634-62
2	643	40.3	300	2	US-09-393-634-58
3	614.5	38.5	317	2	US-09-393-634-60
4	534.5	33.5	333	2	US-09-393-634-3
5	534	33.4	318	2	US-09-393-634-47
6	534	33.4	318	2	US-09-949-016-9253
7	497.5	31.2	312	2	US-09-393-634-51
8	480	30.1	144	2	US-09-393-634-66
9	465	29.1	309	2	US-09-393-634-49
10	463	29.0	307	2	US-09-393-634-53
11	459	28.7	129	2	US-09-393-634-72
12	459	28.7	300	2	US-09-393-634-19
13	448	28.1	300	2	US-09-393-634-17
14	440.5	27.6	316	2	US-09-393-634-39
15	440.5	27.6	316	2	US-09-949-016-8207
16	429	26.9	121	2	US-09-393-634-70
17	426.5	26.7	310	2	US-09-393-634-7
18	417.5	26.1	315	2	US-09-393-634-56
19	395.5	24.8	266	2	US-09-393-634-15
20	335.5	20.9	180	2	US-09-393-634-33
21	326	20.4	299	2	US-09-393-634-35
22	320.5	20.1	299	2	US-09-393-634-43
23	320.5	20.1	299	2	US-09-949-016-6942
24	320.5	20.1	299	2	US-09-949-016-8156
25	314.5	19.7	302	2	US-09-393-634-37
26	307	19.1	224	2	US-09-393-634-9
27	18.6	335	2	2	US-09-393-634-1

28	284	17.8	209	2	US-09-393-634-13	Sequence 13, Appl
29	276.5	17.3	299	2	US-09-393-634-41	Sequence 41, Appl
30	271.5	17.0	299	2	US-09-393-634-5	Sequence 5, Appl
31	263	16.5	291	2	US-09-949-016-8213	Sequence 8213, Ap
32	255	16.0	65	2	US-09-393-634-74	Sequence 74, Appl
33	255	16.0	291	2	US-09-393-634-64	Sequence 64, Appl
34	255	16.0	291	2	US-09-949-016-6919	Sequence 6919, Ap
35	248	15.5	173	2	US-09-393-634-23	Sequence 23, Appl
36	228	14.3	155	2	US-09-393-634-21	Sequence 21, Appl
37	198	12.4	115	2	US-09-393-634-27	Sequence 27, Appl
38	196	12.3	245	2	US-09-393-634-55	Sequence 55, Appl
39	180	11.3	167	2	US-09-949-016-8853	Sequence 8853, Ap
40	177	11.1	126	2	US-09-393-634-31	Sequence 31, Appl
41	151.5	9.5	68	2	US-09-393-634-29	Sequence 29, Appl
42	143	9.0	72	2	US-09-393-634-78	Sequence 78, Appl
43	137	8.6	87	2	US-09-393-634-68	Sequence 68, Appl
44	130.5	8.2	380	1	US-08-153-848-40	Sequence 40, Appl
45	130.5	8.2	380	2	US-09-299-843A-40	Sequence 40, Appl

#### ALIGNMENTS

RESULT 1  
US-09-393-634-62  
; Sequence 62, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 023078-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; CURRENT FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 62  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human GR15  
; NAME/KEY: MOD RES  
; LOCATION: (257)  
; OTHER INFORMATION: Xaa = any amino acid  
US-09-393-634-62

Query Match 69.8%; Score 1115.5; DB 2; Length 300;  
Best Local Similarity 72.2%; Pred. No. 1.4e-105;  
Matches 216; Conservative 34; Mismatches 48; Indels 1; Gaps 1;

Qy	1	MITFLPIIFSSLVVVFVIGNFANGFIALVNSIEWFKEQKISFADQIILTALAVSRVGLLW	60
Db	1	MITFLPIIFSSLVVVFVIGNFANGFIALVNSIEWFKEQKISFADQIILTALAVSRVGLLW	60
Qy	61	VLLLNWSTVLPNAPNSVEVETTAIWIWVNHFSNMLATLISFYLLKIANFSNFIPLH	120
Db	61	VILLHWATVLPNPGSYSLGVATITINAWVNHFSIWATSLISFYFLKIANFSNFIPLH	120
Qy	121	LKRRVKSIVILVMLGLPLFLACHLFPVNNMNIIVTKPEGNNWTKIKLSAMYSFNMTVT	180
Db	121	LKRRIKSVIPVILLGSLFLVCHLVVNMDSMMTKKEYEGNVSWIKLSDPTHLSDMTVT	180
Qy	181	MVANIIVPPTLLISFMILLICSLCKHLKKMQLHGKSGDPSTKVKHVKALQTVISFLLICAI	240
Db	181	TLANLIPPTLLSLLSLCKHLKKMQLHGKSGDPSTKVKHVKALQTVISFLLFAV	240

QY 241 YELSIMISWSP-GSLENKPVFMFCKAIRFSYPSIHPTILWGNKKLKQTFILSVFQWR 298  
DB 241 YFLSLITSWNRRRLXNEPVLMLSQTTAIYPSFHSFILWGSKKLKQTFILLILCQIK 299

## RESULT 2

US-09-393-634-58  
; Sequence 58, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 02307E-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; CURRENT FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 58  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: human GR13  
US-09-393-634-58

Query Match 40.3%; Score 643; DB 2; Length 300;  
Best Local Similarity 46.3%; Pred. No. 2.2e-57;  
Matches 139; Conservative 54; Mismatches 95; Indels 12; Gaps 5;

QY 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
DB 1 MESALPFSITLIIAIFVIGTGLRIMTFIVSNHFNLMATIFSIFLLKIASFSP 60  
QY 61 VLLLNWYSTVLNPAFNSVEVRTAYNI----WAVINHFNSNMLATLSIFYLKIANFSGF 116  
DB 61 ELVSNF---LALHVLAFVSGTGLRIMTFIVSNHFNLMATIFSIFLLKIASFSP 117  
QY 117 IFLHLKRRVKSIVLWMLGPLLFLACHLFINNNEIVRTKEPEGNMTWKIKLSAMYFS- 175  
DB 118 APLYLKRWVNVKILMLLGLTVFLFLNLTIQNNHIKDWLDYERNTTNFNSMDPTFSV 177  
QY 176 --NMTVTWVANLVPETLTLLSFMALICSCLKHKKQLHGKSGDPSSTKVHIKALQTVIS 233  
DB 178 SVKFTWTFP-SUTPTVAFISFLLIFSLQKHLLQKQLNKGHRDPRTKVHTNALKIVIS 236  
QY 234 FLLLCALYFSLMISWMSFGSLNKPVMFCKAIRFSYPSIHPTILWGNKKLKQTFILSV 293  
DB 237 FLLFASFLCLVLIS-WISELQNTVIYMLCETIGVPSSSHFSFLLILGNAKLRQAFLV 295

## RESULT 3

US-09-393-634-60  
; Sequence 60, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 02307E-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; CURRENT FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 60  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: human GR14  
US-09-393-634-60

Query Match 38.5%; Score 614.5; DB 2; Length 317;  
Best Local Similarity 46.2%; Pred. No. 1.9e-54;  
Matches 140; Conservative 52; Mismatches 106; Indels 5; Gaps 4;  
QY 8 IPFSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLWLLNMY 67  
DB 8 IFTFLVIVEFPIGNLGNFIALVNCIDWVKGKISSVDRLITALAIRISLWLIIFSWS 67  
QY 68 STVLNPA-FNSVEVRTAYNIWAVINHFNSNMLATLSIFYLKIANFNFIFLHLKRRVK 126  
DB 68 VSVFPFALFATEKMPRLNTIWTVINHFVSWLATGLGTFFYLKIANFNSIFLYLKWRVK 127  
QY 127 SVILWMLGPLLFLACHLFINNNEIVRTKEPEGNMTWKIKLSAMYFSNMTV--TWVAN 184  
DB 128 KVLVLLLVTSVFLPLNIALININASINGYRRNKTCSDDSNTRFSSLLVLTSTVPI 187  
QY 185 LVPFTLTLLSFMALICSCLKHKKQLHGKSGDPSSTKVHIKALQTVISFLLLCALYFSL 244  
DB 188 FIPFTLSLWMLLIFSNWKKRKKQHTVKISGDASTKAH-RGVKSVITFFLLYALFSL 246  
QY 245 IMISWMSFGSLNKPVMFCKAIRFSYPSIHPTILWGNKKLKQTFILSVFQWRVYVKG 304  
DB 247 FFISVMTSERLEEN-LIILSQVMGWAYPSCHSVLILGNKKLRQASLSVLLWLMFKDG 305  
QY 305 KTS 307  
DB 306 EPS 308

## RESULT 4

US-09-393-634-3  
; Sequence 3, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 02307E-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; CURRENT FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
; FEATURE:  
; OTHER INFORMATION: rat GR02  
US-09-393-634-3

Query Match 33.5%; Score 534.5; DB 2; Length 333;  
Best Local Similarity 41.4%; Pred. No. 3e-46;

Matches	126;	Conservative	52;	Mismatches	107;	Indels	19;	Gaps	4
Qy	9	FSSLVVTFV	TGNGFANGFIALVNSIEWFKOKI	SPADQIL	TALAVSRVGLLWVLLN	WYS	68		
Db	14	FSIIFYVEIV	TGILGNFIALVNMIDWLKRRRI	STADQIL	TALATRLIYVSW	VLICIL	73		
Qy	69	TVLNDAPN	-SVEVRTTAYNIWAVINHFSNWL	ATLSIF	YLLKIANFSNFIF	LHLKRRVKS	127		
Db	74	LFLCPHLS	MRPEMTAIGVIVVDNHF	SIWLATCL	GVFYFLKIASFNS	LSFLYLKWRVKK	133		
Qy	128	VILVWL	GLPLLFLACHLPVINNNEIVR	KEEGNMTWKI	-----	VLKSAMYSNMT	-VTMV	182	
Db	134	VLMII	ILISLIFLMLNTSSGLGMYDHF	SIDVYEGN	SNYLVDS	THPRIFLET	NSKVFEL	193	
Qy	183	AN-----	LVPF	LTLLS	FMLLICSL	CHLKKMQLHGK	SDPSTKVH	229	
Db	194	ANSSHV	FLPNSLFWLIP	FTVSL	VAFFVFL	SLWKHKHKQVNAK	GP	253	
Qy	230	TVISF	LLCAIFYLSIMISVMSFG	SENKPV	FMFC	KAIRFSP	YIPHP	289	
Db	254	IGFSE	LLIYAIYLLFIITGIL	NLDLMRC	IVILL	FDHISG	AVFSISHS	313	
Qy	290	FLSV	293						
Db	314	TL	SV	317					

RESULT 5  
US-09-393-634-47  
; Sequence 47, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 02307E-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; CURRENT FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human GR07  
US-09-393-634-47

	Query Match	33.4%	Score 534;	DB 2;	Length 318;
	Best Local Similarity	40.0%;	Pred. No. 3.2e-46;		
	Matches 123;	Conservative	58;	Mismatches 109;	Indels 16; Gaps 6;
Qy	12	LVVVTFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLWVLLWNYSTVL	71		
Db	12	LAVGEFVGILGNAFIGLVNCDWVKRKIASIDILTSLAISRICLLCVILLDCFTLVL	71		
Qy	72	NPANSV--EVRTTAYNIWAVINHFNSNWLATTLISFYLLKIANFSNFIHLKLRVRSVI	129		
Db	72	YPDVYATGKEMRIIDP--FWLTNHLISWFCLSIYYFFKIGNFPHPLFLWKKWRIDRVI	130		
Qy	130	LVMLLGPILLFLACHLFVI-----NNNE-----IVRTKEPEGNTWKIKLKSAMYSNMTVT	180		
Db	131	SWILLGCVWL---SVFISLPATENLNADRFECVAKR--KTTLTWSRCVNKTOHASTKLFL	186		
Qy	181	MVANLVPFTTLTLLGSFMLLICSLCKHLKQWLHGKSGDPPSPKVHIKALQTVISFLLLCAL	240		

Db	187	NIATLLEPCVCLMSFFLILSLRHHRRMQLSATGCRDPSTENHVRAUKAVITSFLLFLFTA	246
Qy	241	YFLSIMTSVMSFGSLENNKPVMPFCKAIRFSYPSIHFFILLIWNKKLKKOTFLSVFQMRVW	300
Db	247	YYLSFLIATSYFMPETELAVIFGESHIALIYPSHSHFILLIGNNKLRLHASLKVWKMVSI	306
Qy	301	VKGEK	305
Db	307	LKGRK	311

```

RESULT 6
US-09-949-016-9253
; Sequence 9253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9253
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9253

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Query Match      33.4%; Score 534; DB 2; Length 318;
Best Local Similarity 40.0%; Pred. No. 3.2e-46;
Matches 122; Conservative 58; Mismatches 109; Indels 16; Gaps 6;

Qy      12 LVVTVFVIGNFANGFIALVNSIEFKQKISFADQILTALAVSRVGLLVALLNNMYSTVL 71
Db      12 LAVGEFSVGLIGNAFIGLVNCDMWVKRKIASIDILTSLAISRLCLLCVILDDCFILVL 71

Qy      72 NPAFNSV--EVRTTAYNIWAVINHFNSNWLATTLISFYLLKIANFSNFIFHLKRRVKSI 129
Db      72 YPDVYATGKEMRIIDP-FWTLTNHLSIWFATCLSIYFYEKIGNFPHPLFWKWKRIDRVI 130

Qy      130 LVMLLGPILLFLUACHLFWI-----NNNE-----IVTKBEPEGNTWKIKUKSAMYFSNMVT 180
Db      131 SWILLGCVWL---SVFISLPATENLNADRFRCVKAKR-KTLLTWSRCVNKTOHQASTKFL 186

Qy      181 MVANLVFPTLTLLSFMILLICSLCKHLKXQQLHGKSGDPSIKVHIKALQTVISFLLICAI 240
Db      187 NLATLLPFCVCLMSFFLLILSLRHRRMQLSATGCRDPSTEAHVRAUKAVISFLLLFTA 246

Qy      241 YFLSIMITSVMSFGSLENKPFVPMFCARFSYPSIHPFILIIGNKKLKQTFLSVFQMWRYW 300
Db      247 YYLSFLATSSYPMFPETELAVIFGESIALIYPSHSHFILLIGNKKLRHASLKVWIKWSI 306

Qy      301 VKGEK 305
Db      307 LKGEK 311

```

RESULT 7  
US-09-393-634-51  
; Sequence 51, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: zucker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick

```
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 023078-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR09
US-09-393-634-51

Query Match      31.2%; Score 497.5; DB 2; Length 312;
Best Local Similarity 36.6%; Pred. No. 1.6e-42;
Matches 118; Conservative 59; Mismatches 122; Indels 23; Gaps 5;

QY 1 MITELPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
Db 1 MPEATEYIIILAGELTIGWNGFVLVNCIDMLKRDLSLIDIIILSLAISRICLLC 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYN-IWAVINHFSNMLATLSIFYLKIANFSNFIFL 119
Db 61 VISLDGFFMLLPFGTYGNSVLVSIVNVWTPANNSSLWFTSCLSIFYLKIANISHPFF 120

QY 120 HLKRRVSVILVMLGPLLFLF-----LACHLFVNMMNEIVRTKEFEGNWTWKIL 168
Db 121 WLKIKINKYMLAILGSLFSLISIVPKNDMMWYHLFKVSHBE-----NITWKFV 171

QY 169 -KSAMVFSNMTVMVANLVPFTLLSFMLLCSLCKHLKQMLHKGSDPSTKVHIKA 227
Db 172 SKIPGTGKQLTUNL-GVWVPFLICLSIFLLFSLVHTKQIRLHATFRDSTAHWA 230

QY 228 LQTIVSFLLLCIAIYFLSIVMSVSGSLNKPVMFKCAIRFSPSIHPFILGNKKIK 287
Db 231 IKAVIIFLLLIIVYVPVFLVMTSSALIPQGLVLMIGDIVTVIIPSSHSFILMGNSKL 290

QY 288 QTFSLVFWQRYWVKGKTSPP 309
Db 291 EAFKMLRFVKCFLRRKPFVP 312
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```
RESULT 8
US-09-393-634-66
; Sequence 66, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 023078-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
; FEATURE:
; OTHER INFORMATION: human GR17
; NAME/KEY: MOD_RES
; LOCATION: (54)
; OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-66

Query Match      30.1%; Score 480; DB 2; Length 144;
Best Local Similarity 66.9%; Pred. No. 3.6e-41;
Matches 95; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 8 IFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLWLLNMY 67
Db 2 ILSILVFAVLGNVANGFIALVNVNDWVKTKSSSTQIVTALAFSRLGLLXILLHWY 61

QY 68 STVLNPAFNSVEVRTTAYNIWAVINHFSNMLATLSIFYLKIANFSNFIFLHLKRRVK 127
Db 62 ATVFNSALYSLEVRIVPSNVSAIINHFSIWLATLSIFYLKIANFSNFIFLHLKRIKS 121

QY 128 VILVMLGPLLFLACHLFVINM 149
Db 122 VLLVILLGSLVFLICNLAVVTM 143

RESULT 9
US-09-393-634-49
; Sequence 49, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 023078-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR08
US-09-393-634-49

Query Match      29.1%; Score 465; DB 2; Length 309;
Best Local Similarity 35.2%; Pred. No. 3.3e-39;
Matches 103; Conservative 69; Mismatches 109; Indels 12; Gaps 3;

QY 8 IFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLWLLNMY 67
Db 8 IFILITGEFTIGLNGYIALVNVNDWIKKKISTVDYILTNLVIARICLISVMVNGI 67

QY 68 STVLNPAFNSVEVRTTAYNIWAVINHFSNMLATLSIFYLKIANFSNFIFLHLKRRVK 126
Db 68 VIVLNPDYTKNQKQIVFTFTWFANYLNMMITTCNLVYFLKIASSSHPLFLWKWKID 127

QY 127 SVILVMLGPLLFLACHLFVINMMNEIVRTKGF-----EGNWTWKILKSAMVFSNMT 178
Db 128 MVVHWILLG---CFAISLLVSLIAIVLSVCDYRFRHAIKHKENITEMFHVSKIPFEPLT 184

QY 179 VTMVANLVPFTLLSFMLLCSLCKHLKQMLHKGSDPSTKVHIKALQTVISFLLLC 238
Db 185 LFNLPVIFVFLISLISFLLVRLSRHRTKQIKLYATGSRDPSDEVHVAIKNTWTFIFFF 244

QY 239 AIYFLSIMSVMSFGSLNKPVMFKCAIRFSPSIHPFILGNKKLQKTEL 291
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Db 68 AKLFYPSKYFSSLSLEIISY-IMTVNHLTWFAISLSIFVFLKIANFSDCVFLWKERT 126  
QY 126 KSVILVMLGPLL--FLACHLFI-----NNNEIVRTKEPEGNTWKILKLSAMY-PSN 176  
Db 127 DKA-FVFLGCLLTSSWISFSPVVMKDGKVNHNRTSE-----MYWEKROFTINYVFLN 181  
QY 177 MTTVMVANLVPFTLLSPMLLICSCLKHLKQMLHGKSQDPSTKVHIKALQTVISPLL 236  
Db 182 IGVISL-----FMWTLTACFLIMSLWRHSROMQSGVGFRLNTEAHVKAIFLISFI 236  
QY 237 LCATYFLSIMITSVMSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVPWQ 296  
Db 237 LFVLVFIGVSIIEICIFIPENKLLIFGFTTASIYPCCHSFILILNSQLKQAFVKVLQ 296  
QY 297 MRYW 300  
Db 297 LKFF 300  
RESULT 13  
US-09-393-634-17  
; Sequence 17, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: SP, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 02307E-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: mouse GR04  
US-09-393-634-17

Query Match 28.1%; Score 448; DB 2; Length 300;  
Best Local Similarity 33.3%; Pred. No. 1.7e-37;  
Matches 101; Conservative 66; Mismatches 126; Indels 10; Gaps 3;  
QY 1 MITFLPIIPSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLW 60  
Db 1 MLSALESILLSVATSEAMGLVGLNTFIVLVNVDVRNKKLSKINFILTLAISRIFTW 60  
QY 61 VLLLNWYS-----TVLNPAFNSVEVRTTAYNTWAVINHSNWLATLSIFYLLKIANFSN 115  
Db 61 IITLDAYTKVFLTLMLPFS-----SLHECMYSYIWINHLSVWFSTSLGIFVFLKIANFSH 116  
QY 116 FIFLHKRVRKSVILVMLGLPLLFLACHLFLVNMMNEIVRTKEFEGNTWKILKLSAMYFS 175  
Db 117 YIFLWKKRADKV-FVFLIVFLIITWLASFPVAVKVDVKIYQNTSWLHLESELLI 175  
QY 176 NMTVTVANLVPFTLLSPMLLICSCLKHLKQMLHGKSQDPSTKVHIKALQTVISPL 235  
Db 176 NYVFANMGPISLFIIVAIACFLITSLWRHSROMQSGVGFRLNTEAHMKAMKVIAP 235  
QY 236 LCATYFLSIMITSVMSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVPW 295  
Db 236 ILFIFYLGILITETCLFETNNKLLIFGFTTASIMYPCCHSFILILTSRELKQDTMRALQ 295  
QY 296 QMR 298

Db 296 RLK 298  
RESULT 14  
US-09-393-634-39  
; Sequence 39, Application US/09393634  
; Patent No. 6558910  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: SP, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 02307E-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human GR03  
US-09-393-634-39  
Query Match 27.6%; Score 440.5; DB 2; Length 316;  
Best Local Similarity 37.0%; Pred. No. 1.1e-36;  
Matches 108; Conservative 56; Mismatches 117; Indels 11; Gaps 5;  
QY 8 IFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLWVLLNMY 67  
Db 8 VFLILSGTQFTLIGILVNCFIELVNGSSWFKTRMSLSDFIITLALLRILLCIILTDSF 67  
QY 68 STVLNPAFNSVEVRTTAYNI-WAVINHSNWLATLSIFYLLKIANFSNFIPLHLKRRVK 126  
Db 68 LIEFSPNTHDSGIIMQIIDVSWTFNHLISWLATCLGVLYCLKIASFSHPFLMLKWRVS 127  
QY 127 SVILVMLGLPLLFLACHLFLVNMMNEIVRTKEFEG-----NMTWKILKLSAMYFSNVTM 181  
Db 128 RVWVMLLGLL-LSCGSTASLINEFVKLYSVRGIEATRNVTHEHFKRSEYILHVLGT 186  
QY 182 VANLVPFTLLSPMLLICSCLKHLKQMLHGKSQDPSTKVHIKALQTVISFLLLCAY 241  
Db 187 LWYLPPLIVSLASVLLIFSLGRHTRQMLQNGTSRDTTEAHKRAIRIILSFPLFLY 246  
QY 242 FLSIMISVMSFGLS--ENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTF 291  
Db 247 FLAPLIA--SPGNFLPKTKMAKMGIVMTMFYPAGHSFILILGNSKLKQTFV 296  
RESULT 15  
US-09-949-016-8207  
; Sequence 8207, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498



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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:18:56 ; Search time 121 Seconds  
(without alignments)  
1067.019 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MITFLPIFSSLVVTVFVIG.....FLSVFQMRVVKGTSSP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1597	100.0	309	3	US-09-825-882-8
2	1597	100.0	309	4	US-10-017-161-1836
3	1597	100.0	309	4	US-10-191-058-5
4	1597	100.0	309	4	US-10-292-798-1492
5	1597	100.0	309	4	US-10-343-650A-682
6	1597	100.0	309	4	US-10-724-208-8
7	1597	100.0	309	4	US-10-724-208-8
8	1597	100.0	309	5	US-10-724-209-8
9	1597	100.0	309	5	US-10-986-871-8
10	1440	90.2	309	3	US-09-825-882-20
11	1440	90.2	309	4	US-10-017-161-1932
12	1440	90.2	309	4	US-10-292-798-1584
13	1440	90.2	309	4	US-10-724-208-20
14	1440	90.2	309	5	US-10-724-209-20
15	1440	90.2	309	5	US-10-986-871-20
16	1438	90.0	309	4	US-10-770-127-191
17	1424	89.2	309	3	US-09-825-882-12
18	1424	89.2	309	4	US-10-219-834-18
19	1424	89.2	309	4	US-10-017-161-1838
20	1424	89.2	309	4	US-10-292-798-1494
21	1424	89.2	309	4	US-10-343-650A-692
22	1424	89.2	309	4	US-10-724-208-12
23	1424	89.2	309	4	US-10-770-127-183
24	1424	89.2	309	5	US-10-724-209-12
25	1424	89.2	309	5	US-10-986-871-12
26	1348	84.4	299	3	US-09-510-332-76
27	1348	84.4	299	4	US-10-292-798-1480

28	1348	84.4	299	4	US-10-343-650A-670	Sequence 670, Appl
29	1348	84.4	299	4	US-10-770-127-76	Sequence 76, Appl
30	1348	84.4	299	5	US-10-962-365-76	Sequence 76, Appl
31	1334	83.5	299	4	US-10-017-161-1824	Sequence 1824, Ap
32	1299	81.3	319	4	US-10-017-161-1826	Sequence 1826, Ap
33	1299	81.3	319	4	US-10-292-798-1482	Sequence 1482, Ap
34	1293	81.0	319	3	US-09-510-332-70	Sequence 3, Appl
35	1293	81.0	319	4	US-10-191-058-3	Sequence 668, Appl
36	1293	81.0	319	4	US-10-343-650A-668	Sequence 70, Appl
37	1293	81.0	319	4	US-10-770-127-70	Sequence 70, Appl
38	1293	81.0	319	5	US-10-962-365-70	Sequence 56, Appl
39	1285	80.5	309	3	US-09-510-332-56	Sequence 56, Appl
40	1285	80.5	309	5	US-10-962-365-56	Sequence 56, Appl
41	1273	79.7	309	4	US-10-770-127-56	Sequence 53, Appl
42	1215	76.1	299	3	US-09-510-332-53	Sequence 53, Appl
43	1215	76.1	299	4	US-10-770-127-53	Sequence 53, Appl
44	1215	76.1	299	5	US-10-962-365-53	Sequence 53, Appl
45	1185	74.2	319	3	US-09-510-332-51	Sequence 51, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-825-882-8  
; Sequence 8, Application US/09825882  
; Patent No. US20020094551A1  
; GENERAL INFORMATION:  
; APPLICANT: ADLER, JON ELLIOT  
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME  
; FILE REFERENCE: 078003/0279152/RXT  
; CURRENT APPLICATION NUMBER: US/09/825,882  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195,532  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/247,014  
; PRIOR FILING DATE: 2000-11-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-825-882-8

Query Match	100.0%;	Score	1597;	DB	3;	Length	309;
Best Local Similarity	100.0%;	Pred. No.	5.9e-139;				
Matches	309;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKROKISPADQILTALA	VS	RVGLLW	60		
Db	1	MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKROKISPADQILTALA	VS	RVGLLW	60		
Qy	61	VLLNWTSTVLNPAFNSVEVTRTAYNIWAVINHPNSMLATLSIFLLKIANFSNFI	PLH	120			
Db	61	VLLNWTSTVLNPAFNSVEVTRTAYNIWAVINHPNSMLATLSIFLLKIANFSNFI	PLH	120			
Qy	121	LKRRVKSIVLLMGLPPLLFLACHLFINNMEIVRTKEFGNMTWKIKLSAMYFSNMTVT	180				
Db	121	LKRRVKSIVLLMGLPPLLFLACHLFINNMEIVRTKEFGNMTWKIKLSAMYFSNMTVT	180				
Qy	181	MVANLVPFTLLSFMILLISLCKHLKQNLHGKSGDPSPTKVHICALQTVISFLLCAI	240				
Db	181	MVANLVPFTLLSFMILLISLCKHLKQNLHGKSGDPSPTKVHICALQTVISFLLCAI	240				
Qy	241	YFLSIMISVMSFGSLENKPKVFMCKAIRFSYPSHPILLINGNKKLQTPFLSVFQWQRYW	300				
Db	241	YFLSIMISVMSFGSLENKPKVFMCKAIRFSYPSHPILLINGNKKLQTPFLSVFQWQRYW	300				
Qy	301	VKGEKTSPP	309				
Db	301	VKGEKTSPP	309				

RESULT 2  
US-10-017-161-1836  
; Sequence 1836, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1836  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-1836

Query Match 100.0%; Score 1597; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 5.9e-139;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60  
Db 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60

Qy 61 VLLLNWYSTVLNPAFNSVEVETTAIYNIWAVINHFNSNWLATTLSIFYLKIANFSNFIPLH 120  
Db 61 VLLLNWYSTVLNPAFNSVEVETTAIYNIWAVINHFNSNWLATTLSIFYLKIANFSNFIPLH 120

Qy 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180  
Db 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180

Qy 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240  
Db 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240

Qy 241 YFLSTMISVWSEGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300  
Db 241 YFLSTMISVWSEGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300

Qy 301 VKGEKTSPP 309  
Db 301 VKGEKTSPP 309

RESULT 3  
US-10-191-058-5  
; Sequence 5, Application US/10191058  
; Publication No. US20030170608A1  
; GENERAL INFORMATION:  
; APPLICANT: PRONIN, ALEXEY  
; APPLICANT: CONNOR, JUDY  
; APPLICANT: TANG, HUIXIAN  
; APPLICANT: KEUNG, WALTER  
; APPLICANT: SERVANT, GUY  
; APPLICANT: ADLER, JON ELLIOT  
; APPLICANT: O'CONNELL, SHAWN  
; APPLICANT: BRUST, PAUL  
; TITLE OF INVENTION: USE OF SPECIFIC T2R TASTE RECEPTORS TO IDENTIFY  
; FILE REFERENCE: 078003-0280784  
; CURRENT APPLICATION NUMBER: US/10/191,058  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: 60/303,811  
; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/372,089  
; PRIOR FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-191-058-5

Query Match 100.0%; Score 1597; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 5.9e-139;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60  
Db 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60

Qy 61 VLLLNWYSTVLNPAFNSVEVETTAIYNIWAVINHFNSNWLATTLSIFYLKIANFSNFIPLH 120  
Db 61 VLLLNWYSTVLNPAFNSVEVETTAIYNIWAVINHFNSNWLATTLSIFYLKIANFSNFIPLH 120

Qy 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180  
Db 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180

Qy 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240  
Db 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKGSQDPSTKVHIKALQTVISFLLCAI 240

Qy 241 YFLSTMISVWSEGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300  
Db 241 YFLSTMISVWSEGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300

Qy 301 VKGEKTSPP 309  
Db 301 VKGEKTSPP 309

RESULT 4  
US-10-292-798-1492  
; Sequence 1492, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1492  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-1492

Query Match 100.0%; Score 1597; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 5.9e-139;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60  
Db 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60

Qy 61 VLLLNWYSTVLNPAFNSVEVETTAIYNIWAVINHFNSNWLATTLSIFYLKIANFSNFIPLH 120

Db 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120  
Qy 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
Db 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
Qy 181 MVANLVPPTLLTLLSFMLLICSCKHLKKMQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240  
Db 181 MVANLVPPTLLTLLSFMLLICSCKHLKKMQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240  
Qy 241 YFLSIMISVWFSGLSKENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFWQMRYW 300  
Db 241 YFLSIMISVWFSGLSKENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFWQMRYW 300  
Qy 301 VKGEKTSSP 309  
Db 301 VKGEKTSSP 309

## RESULT 5

US-10-343-650A-682  
; Sequence 682, Application US/10343650A  
; Publication No. US20040067499A1  
; GENERAL INFORMATION:  
; APPLICANT: HAGA, TATSUYA  
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: 31671-186347  
; CURRENT APPLICATION NUMBER: US/10/343,650A  
; CURRENT FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: JP 2000/237818  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: JP 2001/34434  
; PRIOR FILING DATE: 2001-02-13  
; NUMBER OF SEQ ID NOS: 694  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 682  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-343-650A-682

Query Match 100.0%; Score 1597; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 5.9e-139;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
Db 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
Qy 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120  
Db 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120  
Qy 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
Db 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
Qy 181 MVANLVPPTLLTLLSFMLLICSCKHLKKMQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240  
Db 181 MVANLVPPTLLTLLSFMLLICSCKHLKKMQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240  
Qy 241 YFLSIMISVWFSGLSKENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFWQMRYW 300  
Db 241 YFLSIMISVWFSGLSKENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFWQMRYW 300  
Qy 301 VKGEKTSSP 309  
Db 301 VKGEKTSSP 309

## RESULT 6

US-10-724-208-8

; Sequence 8, Application US/10724208  
; Publication No. US20040209313A1  
; GENERAL INFORMATION:  
; APPLICANT: ADLER, JON ELLIOT  
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME  
; FILE REFERENCE: 078003/0279152/RXT  
; CURRENT APPLICATION NUMBER: US/10/724,208  
; CURRENT FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: 60/195,532  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/247,014  
; PRIOR FILING DATE: 2000-11-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-724-208-8

Query Match 100.0%; Score 1597; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 5.9e-139;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
Db 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60  
Qy 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120  
Db 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120  
Qy 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
Db 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180  
Qy 181 MVANLVPPTLLTLLSFMLLICSCKHLKKMQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240  
Db 181 MVANLVPPTLLTLLSFMLLICSCKHLKKMQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240  
Qy 241 YFLSIMISVWFSGLSKENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFWQMRYW 300  
Db 241 YFLSIMISVWFSGLSKENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFWQMRYW 300  
Qy 301 VKGEKTSSP 309  
Db 301 VKGEKTSSP 309

## RESULT 7

US-10-770-127-179  
; Sequence 179, Application US/10770127  
; Publication No. US20040214239A1  
; GENERAL INFORMATION:  
; APPLICANT: SERVANT, GUY  
; APPLICANT: OZECK, MARK  
; APPLICANT: BRUST, PAUL  
; APPLICANT: XU, HONG  
; TITLE OF INVENTION: FUNCTIONAL COUPLING OF T1RS AND T2RS BY GI PROTEINS  
; TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF T1R  
; FILE REFERENCE: 100337.54281US  
; CURRENT APPLICATION NUMBER: US/10/770,127  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: 60/444,172  
; PRIOR FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: 60/457,318  
; PRIOR FILING DATE: 2003-03-26  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 179  
; LENGTH: 309  
; TYPE: PRT



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; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 309
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-825-882-20

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Query Match 90.2%; Score 1440; DB 3; Length 309;  
Best Local Similarity 88.3%; Pred. No. 1.8e-124;  
Matches 272; Conservative 20; Mismatches 16; Indels

Qy	1	MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW	60
Db	1	MITFLPIIFSILVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW	60
Qy	61	VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHPSNWLATTSIFYLLKIANFSNFIPLH	120
Db	61	VLVLNWYATELNPAFNSIEVRTAYNVWAVINHPSNWLATLSIFYLLKIANFSNLIPLH	120
Qy	121	LKRVRKSVLLVMLGLPLLFLACHLPVNNNETVTRKEPEGNNWTIKLKSAFYFSNMTVT	180
Db	121	LKRVRKSVVLVLGLPLLFLVCHLPVNNNQIITWKEYEGNNWTIKURSAMYLSNNTVT	180
Qy	181	MVANLVPTTLTLLSFMLLICSLCKHLKKMQLHGKSGDPSTKVHIIKALQTVISFLLLCAI	240
Db	181	ILANLVPTTLTLLSFLLLICSLCKHLKKMQLHGKSGDPSPMKVHIIKALQTVISFLLLCAI	240
Qy	241	YFLSIMISVMSFGSLENKPVFMFCKAIRFSYPSIHPFILIIGNKKLKTFTLSVFWMQRYW	300
Db	241	YFLSIIINSVMSFSELENKPVFMFCEAIFAISYPSIHPFILIIGNKKLKTFTLSVLHVRVY	300
Qy	301	VKEKTS 308	
Db	301	VKEKPS 308	

RESULT 11

```

US-10-017-161-1932
/ Sequence 1932, Application US/10017161
/ Publication NO. US20030143668A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ASURATANI, HIROYUKI
/ TITLE OF INVENTION: NOVEL G PROTEIN-C
/ FILE REFERENCE: 084335/0152
/ CURRENT APPLICATION NUMBER: US/10/017
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: JP 2001/246
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2430
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1932
/ LENGTH: 309
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-017-161-1932

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Query Match      90.2%; Score 1440; DB 4; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITPLPIPSLSVVTVVIGNFANGFIALVNSIEWFKRKQKISPADQILTALAVSRVGLLW 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MITPLPIPSLSIIIVTVVIGNFANGFIALVNSIEWFKRKQKISPADQILTALAVSRVGLLW 60

QY 61 VLLINWYSTVLINPAFNSVEVRTTAINTWAVINHPNSNWLATLTLSFYLLKLTANFNSNFI 120

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Db      61 VLVLNWTATELNPAPFNSIEVRITAYNWAVINHFSNMLATSLSFYLLKIANFSNLIFLH 120
Qy     121 LKRKVSVILVMLGAPLLFLACLHLFVINMNEIVRTKEPEGNTWKIKLKSA MYFSNMVT 180
Db     121 LKRKVSWLVLILGAPLLFLVCHLFVINMNQIIWTKKEYEGNTWKIKLRSAM YLSNTT 180
Qy     181 MVANLVPTTTLLSPFMILLICSLCKHLKKOQLHGSGSDPSKTVHIKALQT VISP LLCAI 240
Db     181 ILANLVPTTTLISFLGLICSLCKHLKKOQLHGSGQDPSMKVHIKALQT VTS FL LCAI 240
Qy     241 YFLSIMISVMVSGSLENKPVMFCKAIRFSYPSHPFFILIWNKKLKOTFL SVFWOMRYW 300
Db     241 YFLSIIMVMSVFESLENKPVMFCFAIFSYPSTHPFFILIWNKKLKOTFL SVLWHVRYW 300
Qy     301 VKGEKTSS 308
Db     301 VKGEKPSS 308

RESULT 12
US-10-292-798-1584
; Sequence 1584, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1584
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-1584
```

[illegible]

```
RESULT 13
US-10-724-208-20
; Sequence 20, Application US/10724208
; Publication No. US20040209313A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/724,208
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-724-208-20

Query Match      90.2%; Score 1440; DB 4; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITPLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIIFSSILIVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLNMYSTVLNPAFNSIEVVRTTAYNIWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
DB 61 VLVLNMYATELNPAPNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNLIPLH 120
QY 121 LKRRVKSIVLVMILGPLLFLACHLFLVINNMNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVILLGPLLFLVCHLFLVINNMNQIITWKEYEGNNTWKIKLSAMYSNMTVT 180
QY 181 MVANLVPTLTLLSFMLLICSLCKHLKMQQLHGKGSQDPSSTKVHIKALQTVTSFLLLCAL 240
DB 181 ILANLVPTLTLLSFLLILCSLCKHLKMQQLHGKGSQDPSMKVHIKALQTVTSFLLLCAL 240
QY 241 YFLSIMISVWSFSGLENKPVFMFCFAIRPSYPSIHPFILIWGNKKLKQTFLSVFMQMYW 300
DB 241 YFLSIIMSWSFSELENKPVFMFCFAIAFSYPSHPFILIWGNKKLKQTFLSVLMHVRYW 300
QY 301 VKGEKTSS 308
DB 301 VKGEKPSS 308

RESULT 14
US-10-724-209-20
; Sequence 20, Application US/10724209
; Publication No. US20040248149A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 100337.54075US
; CURRENT APPLICATION NUMBER: US/10/724,209
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-724-209-20

Query Match      90.2%; Score 1440; DB 4; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITPLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIIFSSILIVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLNMYSTVLNPAFNSIEVVRTTAYNIWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
DB 61 VLVLNMYATELNPAPNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNLIPLH 120
QY 121 LKRRVKSIVLVMILGPLLFLACHLFLVINNMNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVILLGPLLFLVCHLFLVINNMNQIITWKEYEGNNTWKIKLSAMYSNMTVT 180
QY 181 MVANLVPTLTLLSFMLLICSLCKHLKMQQLHGKGSQDPSSTKVHIKALQTVTSFLLLCAL 240
DB 181 ILANLVPTLTLLSFLLILCSLCKHLKMQQLHGKGSQDPSMKVHIKALQTVTSFLLLCAL 240
QY 241 YFLSIMISVWSFSGLENKPVFMFCFAIRPSYPSIHPFILIWGNKKLKQTFLSVFMQMYW 300
DB 241 YFLSIIMSWSFSELENKPVFMFCFAIAFSYPSHPFILIWGNKKLKQTFLSVLMHVRYW 300
QY 301 VKGEKTSS 308
DB 301 VKGEKPSS 308
```

```
Query Match      90.2%; Score 1440; DB 5; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITPLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIIFSSILIVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLNMYSTVLNPAFNSIEVVRTTAYNIWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
DB 61 VLVLNMYATELNPAPNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNLIPLH 120
QY 121 LKRRVKSIVLVMILGPLLFLACHLFLVINNMNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVILLGPLLFLVCHLFLVINNMNQIITWKEYEGNNTWKIKLSAMYSNMTVT 180
QY 181 MVANLVPTLTLLSFMLLICSLCKHLKMQQLHGKGSQDPSSTKVHIKALQTVTSFLLLCAL 240
DB 181 ILANLVPTLTLLSFLLILCSLCKHLKMQQLHGKGSQDPSMKVHIKALQTVTSFLLLCAL 240
QY 241 YFLSIMISVWSFSGLENKPVFMFCFAIRPSYPSIHPFILIWGNKKLKQTFLSVFMQMYW 300
DB 241 YFLSIIMSWSFSELENKPVFMFCFAIAFSYPSHPFILIWGNKKLKQTFLSVLMHVRYW 300
QY 301 VKGEKTSS 308
DB 301 VKGEKPSS 308

RESULT 15
US-10-986-871-20
; Sequence 20, Application US/10986871
; Publication No. US20050069944A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/986,871
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/825,882
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-871-20

Query Match      90.2%; Score 1440; DB 5; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITPLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIIFSSILIVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLNMYSTVLNPAFNSIEVVRTTAYNIWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
DB 61 VLVLNMYATELNPAPNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNLIPLH 120
QY 121 LKRRVKSIVLVMILGPLLFLACHLFLVINNMNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVILLGPLLFLVCHLFLVINNMNQIITWKEYEGNNTWKIKLSAMYSNMTVT 180
QY 181 MVANLVPTLTLLSFMLLICSLCKHLKMQQLHGKGSQDPSSTKVHIKALQTVTSFLLLCAL 240
DB 181 ILANLVPTLTLLSFLLILCSLCKHLKMQQLHGKGSQDPSMKVHIKALQTVTSFLLLCAL 240
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Qy	241	YFLSIMISVMSFGSLENKPVFMFCCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMYW	300
Db	241	YFLSIMISVMSFGSLENKPVFMFCCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMYW	300
Qy	301	VKGEKTS	308
Db	301	VKGEKPSS	308

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Job time : 122 secs

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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:19:46 ; Search time 44 Seconds  
(without alignments)  
319.379 Million cell updates/sec

Title: US-09-825-882-8  
Perfect score: 1597  
Sequence: 1 MITFLPIFSLVVFVIG.....FLSVFMQRYVWVGKTSPP 309

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA New:\*
- 1: /SID55/prodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
  - 2: /SID55/prodata/1/pubpaa/US06\_NEW\_PUB.pap.\*
  - 3: /SID55/prodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
  - 4: /SID55/prodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*
  - 5: /SID55/prodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
  - 6: /SID55/prodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
  - 7: /SID55/prodata/1/pubpaa/US11\_NEW\_PUB.pap.\*
  - 8: /SID55/prodata/1/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	695	43.5	148	7	US-11-264-096-1287
2	459	28.7	307	7	US-11-264-096-688
3	388	24.3	111	7	US-11-000-463-330
4	388	24.3	111	7	US-11-000-463-802
5	287	18.0	63	7	US-11-264-096-860
6	278	17.4	318	7	US-11-182-942-2
7	242	15.2	181	7	US-11-264-096-689
8	130.5	8.2	380	7	US-11-210-139-17
9	123	7.7	360	6	US-10-959-310-36
10	123	7.7	360	7	US-11-144-731-1
11	123	7.7	360	7	US-11-262-284-34
12	116.5	7.3	316	7	US-11-188-298-12382
13	116	7.3	346	6	US-10-455-772-442
14	116	7.3	346	6	US-10-455-772-444
15	116	7.3	346	7	US-11-157-930-2
16	113.5	7.1	318	6	US-10-055-877-324
17	111.5	7.0	310	6	US-10-455-772-124
18	111.5	7.0	313	6	US-10-055-877-234
19	111.5	7.0	316	7	US-11-188-298-9290
20	106.5	6.7	352	7	US-11-028-922A-1
21	105.5	6.6	270	6	US-10-455-772-132
22	105.5	6.6	274	6	US-10-455-772-126
23	105.5	6.6	318	6	US-10-055-877-119
24	105.5	6.6	318	6	US-10-055-877-322
25	105.5	6.6	359	6	US-10-995-561-712

26	105.5	6.6	359	6	US-10-995-561-716	Sequence 716, App
27	105.5	6.6	359	7	US-11-127-877-65	Sequence 65, Appl
28	105.5	6.6	388	6	US-10-995-561-713	Sequence 713, App
29	105.5	6.6	394	6	US-10-995-561-714	Sequence 714, App
30	105.5	6.6	394	6	US-10-995-561-715	Sequence 715, App
31	105.5	6.6	509	7	US-11-098-686-10325	Sequence 10325, A
32	104	6.5	362	7	US-11-079-463-6266	Sequence 6266, Ap
33	103.5	6.5	314	6	US-10-455-772-130	Sequence 130, App
34	103.5	6.5	314	7	US-11-190-188-16	Sequence 16, Appl
35	103.5	6.5	321	6	US-10-455-772-128	Sequence 128, App
36	103.5	6.5	717	7	US-11-096-568A-31003	Sequence 31003, A
37	103.5	6.5	729	7	US-11-096-568A-31002	Sequence 31002, A
38	103	6.4	348	6	US-10-330-773-921	Sequence 921, App
39	102.5	6.4	359	6	US-10-876-787-2	Sequence 2, Appl
40	101	6.3	463	7	US-11-087-099-1578	Sequence 1578, Ap
41	101	6.3	463	7	US-11-045-004-1257	Sequence 1257, Ap
42	100.5	6.3	311	6	US-10-455-772-556	Sequence 556, App
43	100.5	6.3	311	6	US-10-455-772-570	Sequence 570, App
44	100.5	6.3	313	6	US-10-455-772-554	Sequence 554, App
45	100.5	6.3	313	6	US-10-455-772-562	Sequence 562, App

ALIGNMENTS

RESULT 1

US-11-264-096-1287  
; Sequence 1287, Application US/11264096  
; Publication No. US20060084794A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546D1  
; CURRENT APPLICATION NUMBER: US/11/264,096  
; CURRENT FILING DATE: 2005-11-02  
; PRIOR APPLICATION NUMBER: 09/833,245  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229,358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256,931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199,384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1287  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-264-096-1287

Query Match 43.5%; Score 695; DB 7; Length 148;  
Best Local Similarity 89.2%; Pred. No. 8.9e-53;  
Matches 132; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
Qy 162 MTWKIKLSAMVFNMTVTVMANLVPTLTLLSPMLLICSICXHLKXQMLHGKSGQDPST 221  
Db 1 MTWKIKLSAVYLSDATVTTILGNLVPTLTLLCPFLLLICSLCKHLKXQMLHGKSGQDPST 60  
Qy 222 KVHIKALQTVISFLLCAIYFLSTIMISVWSFGSLNKVPMFKCAIRFSPYSHPFILW 281  
Db 61 KVHIKVLQTVIFFLLCAIYFLSTIMISVWSFGSLNKVPMFKCAIRFSPYSHPFILW 120  
Qy 282 GNKKLKQTFLSVFMQRYWVGKTSPP 309  
Db 121 GNKKLKQTFLSVLRQRYWVGKTSPP 148

RESULT 2

US-11-264-096-688  
; Sequence 688, Application US/11264096  
; Publication No. US20060084794A1  
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 688
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (249)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (261)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-11-264-096-688

Query Match      28.7%; Score 459; DB 7; Length 307;
Best Local Similarity 36.1%; Pred. No. 3.6e-32;
Matches 109; Conservative 62; Mismatches 121; Indels 10; Gaps 5;

Qy 1 MTFPLPITSSLVVTVFVGNFANGFIALVNSIEWFKQKISFADQIITALAVSRVGLW 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLRVVEGIFVFWSESVEGLNGFVGLVNCIDCAK-NKLSITIGFILTGLAISRIPLW 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 VLLLNWYSTVLPN---AFNSVEVETTAINTWAVNHFSNMLATTLSIFYLKIANFSNF 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 IITDGTQIFSPNIYAGNLLEY--ISY-FWVIGNQSSMFWFATSLSIYFLKIANFSNY 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 117 IFHLKRRVKSVILVMLGLPLFLACHLFVINMNEIVRTKEPEGNMTWKIKLSAMYFSN 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 IFLWLSKRNWVLPFWIV--FLISSLLNFAYIAKLNDYKMKNDTVMDLNMYKSEYIK 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 177 MVTVMVANLVPTTLFLLSFMLLICSLKHLKQMLHKGSDPSKVKHKKALQTVVISFL 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 QILLNLGVIFFFTLSLITCFILIIISLWRHNRQMSNVTLGRDSNTEAHVKAMKVLISPI 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 237 LCAIYFLSMISVWFGSLKPKVFMCKAIRFSYPSIHPFLIWNKKLKQTLFSVFMQ 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 LPILYFIGNAIEISXFTVRENKLLMXGNTTATYIPWGHSPFILLGNSKLQASLURVLO 294
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 297 MR 298
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Db 295 LX 296

RESULT 3
US-11-000-463-330
; Sequence 330, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Cao, Yi-Cheng
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
```

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; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-000-463-330

Query Match      24.3%; Score 388; DB 7; Length 111;
Best Local Similarity 80.9%; Pred. No. 1.5e-26;
Matches 76; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 209 MOLHGKGSQDSTKVHKKALQTVISFLLLCALYFLSLMISVWFGSLKPKVFMCKAIR 268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MOLHGKGSQDSTKVHKKALQTVISFLLLCALYFLSLMISVWFGSLKPKVFMCKAIR 268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 269 FSYSPHPIILWGNKKLKQTLFSVFMQMYVK 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 FSYSTPHPIILWGNKKLKQTLFSVLRHRYVVK 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
US-11-000-463-802
; Sequence 802, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
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; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 802
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-802

Query Match      24.3%; Score 388; DB 7; Length 111;
Best Local Similarity 80.9%; Pred. No. 1.5e-26;
Matches 76; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 209 MQLHGKSGDSTKVKHIKALQTVISFLLLCAYFLSIMISVMSFGSLNKPVMFCKAIR 268
Db 1 MQLHGKSGDSTKVKHIKALQTVISFLLLCAYFLSIMISVMSFGSLNKPVMFCKAIR 60

Qy 269 FSYPSIHPFLLIWNKKLQKTFSLVFWQMRVYWK 302
Db 61 FSYPSIHPFLLIWNKKLQKTFSLVFWQMRVYWK 94

RESULT 5
US-11-264-096-860
; Sequence 860, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR FILING DATE: 2005-11-02
; PRIOR FILING DATE: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 60/199, 384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 860
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-860

Query Match      18.0%; Score 287; DB 7; Length 63;
Best Local Similarity 93.7%; Pred. No. 4e-18;
Matches 59; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MITFLPIFSLVVVTVIGNFANGFIALVNSIEWFKRKISFADQILITALAVSRVGLLW 60
Db 1 MITFLPIFSLVVVTVIGNFANGFIALVNSIEWFKRKISFADQILITALAVSRVGLLW 60

Qy 61 VLL 63
Db 61 VLL 63

RESULT 6
US-11-182-942-2
; Sequence 2, Application US/11182942
; Publication No. US20060019346A1
; GENERAL INFORMATION:
; APPLICANT: Senomys, Inc.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Tang, Huixian
; APPLICANT: Pronin, Alexey
; TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76
; FILE REFERENCE: 78003-292936
; CURRENT APPLICATION NUMBER: US/11/182,942
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; CURRENT FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-942-2

Query Match      17.4%; Score 278; DB 7; Length 318;
Best Local Similarity 28.1%; Pred. No. 1.3e-16;
Matches 84; Conservative 60; Mismatches 135; Indels 20; Gaps 7;

Qy 7 IIFSLVVTVIGNFANGFIALVNSIEWFKRKISFADQILITALAVSRVGLLWVLLNW 66
Db 18 IILVTILLRLVAIGNGFITAAALGVWEVLRMLPCDKLLVSLGASRFCLQSVVMGKT 77

Qy 67 YSTVLP---AFNSVEVTRTAYINWAVINSHESWMLATTLISFYLLKIANFNSFIHLKR 123
Db 78 IYVFLHPMAFFYFNV-LQFLAQ-WDFLNAATLMSSTWLSVFCVKIATFTHPVFFWLKH 135

Qy 124 RVKSVILVMLGP-----LLFLACHLFIWNNEIVRTKEPEGNMTWKIKLSAMYF 174
Db 136 KLSGLPFWMLFSSVGLSSFTTILFFIGNHMYQN---YLRNHLQPNWVTGDSIRSCEKF 192

Qy 175 SNMTVTWVANLVPTLLSLFMLLISLCKHLKQMLHGKSGDSTKVKHIKALQTVISF 234
Db 193 YLFPKMTITWMTPTAVFFICMILLITSLGRHKALLTTSGRFBSVQAHIKALLALSP 252

Qy 235 LLLCAIYFLSIMISVMS-FGSLNKPVMFCKAIRFSYPSIHPFLLIWNKKLQKTFLS 292
Db 253 AMLFISYFLSLVFSAGIIPPPLDFK--FWWVESVYLCAAVHPITLLFNSCRLRAVLKS 309

RESULT 7
US-11-264-096-689
; Sequence 689, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR FILING DATE: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 689
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-689

Query Match      15.2%; Score 242; DB 7; Length 181;
Best Local Similarity 32.2%; Pred. No. 9.1e-14;
Matches 55; Conservative 40; Mismatches 70; Indels 6; Gaps 1;

Qy 128 VILVMLGLPLFLACHLFIWNNEIVRTKEPEGNMTWKIKLSAMYFSNMTVTWVANLV 187
Db 6 MIVFLLISLNLFA-----YIAKLNDYKDKNDTVWDLNMYKSEYFIKQILLNLGVIF 59

Qy 188 FTLTSLFMLLISLCKHLKQMLHGKSGDSTKVKHIKALQTVISFLLCAIYFLSLMI 247
Db 60 FTLTSLTICFLLISLWHRNQMSNVTLGRSDNTAEHVAKMKVLISFILFILYFIGNAI 119

Qy 248 SVMSFGSLNKPVMFCKAIRFSYPSIHPFLLIWNKKLQKTFLSVFWQMR 298
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Db      : ||| : || | ||| ||| ||| ||| ||| ||| : ||| :
120 EISCVTRENKLLMPGHTTTTAYIPWGHSFILILGNSKQASRLVLOQLK 170

RESULT 8
US-11-210-139-17
; Sequence 17, Application US/11210139
; Publication No. US20060045880A1
; GENERAL INFORMATION:
; APPLICANT: KRIEG, PAUL A.
; TITLE OF INVENTION: METHODS FOR MODULATING ANGIOGENESIS AND APOPTOSIS
; FILE REFERENCE: 20825-0008
; CURRENT APPLICATION NUMBER: US/11/210,139
; CURRENT FILING DATE: 2005-08-23
; PRIOR APPLICATION NUMBER: 60/803,807
; PRIOR FILING DATE: 2004-08-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 17
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-210-139-17

Query Match      8.2%; Score 130.5; DB 7; Length 380;
Best Local Similarity 19.0%; Pred. No. 0.00076;
Matches 66; Conservative 79; Mismatches 125; Indels 77; Gaps 16;

Qy      8 IPSSLVVTVFVIGNFANGFIALVNSIEW-----FKQKISFADQIITALAVSRVGLLWLL 63
Db      30 LIPATYMLVLLGTGNGLVL-----WTVFRSSREKRSADIFIASLAVA--DLTFVVT 81

Qy      64 LNWYSTV-----LNPAFNSVEVTTAYINIAVINHFNLSNLTLSIF--YLLKIANFNSFI 117
Db      82 LPLMATYTVRDYDWPFGTFCKLSVYLIF--VNMYASVFCLTGLSFDRLAIVRPVAN-- 137

Qy      118 FHLKRRVKSVLVMLLGLP-LFLACHLFI--NMNEIVRTKEFEGNM-----T 163
Db      138 -ARLRVSGAVATAVLWLAALLAMPVNLRTTGDLENTTKVQCYMDYSVMVATVSSEWA 196

Qy      164 WKIKLSAMYFNSMTVTWVANLVPTLTLLSPMLLICSILCKHLKQKQHLGKSGQDPSTKV 223
Db      197 NEVGL-----GVSTTVGVVPTIMLTCTYFFTAQIAGHFRKERIEG----- 239

Qy      224 HTKALQTVISFLLCAIYF-----LSMISVMSFGSLENKP-----VFMPCKAIR 268
Db      240 -LRKRRLLSIIVLWLVTFALCMVPYHLVKTLYMLGSLLLHWPDCDFLFLMNIFPYCTCIS 298

Qy      269 PSYPSIHPILLGNKKLKQTFLSVF--WQMR-----YVVKGEKTS 308
Db      299 YVNSCLNPLFYAFFDRFRQACTSMLCCGQSRCACTSHSSGKXSAS 345
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; ORGANISM: Homo sapiens
US-10-959-310-36

Query Match      7.7%; Score 123; DB 6; Length 360;
Best Local Similarity 18.5%; Pred. No. 0.0032;
Matches 63; Conservative 62; Mismatches 105; Indels 110; Gaps 14;

Qy      4 FLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKI-SPADQILTALAVS----- 54
Db      41 FLPLPLYS-----LVFVFGLLGNSVVVLV----LFFVKRLRSMTDYYLLNLAISDLLFVPSL 92

Qy      55 -----RVGLL-----WVLLNMYSTVLNPAFNSVEVTRTAYINIAVINHFNQNM 97
Db      93 PFWGYAAADQWVFGGLGCKMISWMYLVGFYSGIFFVMLMSID-----RYLAIVHAVFSL 146

Qy      98 LATTLSIFYLKIANFNSNFIHLKRRVKSVILVMLGPLLFLACHLFLVINNEIVRTKE 157
Db      147 RARTLTGVITSLATWSVAVFASLP-----GFLFSTC--YTERNHVYCKTKY 191

Qy      158 PEGNMTWKIKLSAMYFNSMTVTWVANLVPTLTLLSPMLLICSIL--CKHLKQKQHLGKG 215
Db      192 SLNSTTWKV-----LSSLEINILGLVIPIGIMLFCYSMIIRTLQHCNKKCN----- 238

Qy      216 SQDPSTKVHIKALQTVISFLLC-----AIYFLSIMISVMSFGSLENKPVFMFC--- 264
Db      239 -----KAVKMIFAVVVLFGFWTPPNIVLFLTELVEL-----EVLQDCTFE 279

Qy      265 -----KAIKRSYPSIHPFILIWNKKLQTFLSVF 294
Db      280 RYLDVAIQATETLAFVHCCLNPIIVFVLGKFKRVILQLF 319

RESULT 10
US-11-144-731-1
; Sequence 1, Application US/11144731
; Publication No. US20060034841A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Method of depleting regulatory T cell
; FILE REFERENCE: 11542US2
; CURRENT APPLICATION NUMBER: US/11/144,731
; CURRENT FILING DATE: 2005-06-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-731-1

Query Match      7.7%; Score 123; DB 7; Length 360;
Best Local Similarity 18.5%; Pred. No. 0.0032;
Matches 63; Conservative 62; Mismatches 105; Indels 110; Gaps 14;

Qy      4 FLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKI-SPADQILTALAVS----- 54
Db      41 FLPLPLYS-----LVFVFGLLGNSVVVLV----LFFVKRLRSMTDYYLLNLAISDLLFVPSL 92

Qy      55 -----RVGLL-----WVLLNMYSTVLNPAFNSVEVTRTAYINIAVINHFNQNM 97
Db      93 PFWGYAAADQWVFGGLGCKMISWMYLVGFYSGIFFVMLMSID-----RYLAIVHAVFSL 146

Qy      98 LATTLSIFYLKIANFNSNFIHLKRRVKSVILVMLGPLLFLACHLFLVINNEIVRTKE 157
Db      147 RARTLTGVITSLATWSVAVFASLP-----GFLFSTC--YTERNHVYCKTKY 191

Qy      158 PEGNMTWKIKLSAMYFNSMTVTWVANLVPTLTLLSPMLLICSIL--CKHLKQKQHLGKG 215
Db      192 SLNSTTWKV-----LSSLEINILGLVIPIGIMLFCYSMIIRTLQHCNKKCN----- 238

Qy      216 SQDPSTKVHIKALQTVISFLLC-----AIYFLSIMISVMSFGSLENKPVFMFC--- 264
Db      239 -----KAVKMIFAVVVLFGFWTPPNIVLFLTELVEL-----EVLQDCTFE 279
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QY 265 -----KAIRFSYPSIHPIILWGNKKLKQTFSLV 294
      : : : : : : : : : : : : : : : : : :
Db 280 RYLDVAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQLF 319

RESULT 11
US-11-262-284-34
; Sequence 34, Application US/11262284
; Publication No. US20060057112A1
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE (MDC), MDC ANALOGS, MDC
; FILE OF INVENTION: INHIBITOR SUBSTANCES, AND USES THEREOF
; FILE REFERENCE: 27866/34810
; CURRENT APPLICATION NUMBER: US/11/262,284
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 09/067,447
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 08/939,107
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 08/660,542
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: 08/558,658
; PRIOR FILING DATE: 1995-11-16
; PRIOR APPLICATION NUMBER: 08/479,620
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens - human CCR4
US-11-262-284-34.

Query Match 7.7%; Score 123; DB 7; Length 360;
Best Local Similarity 18.5%; Pred. No. 0.0032;
Matches 63; Conservative 62; Mismatches 105; Indels 110; Gaps 14;

QY 4 FLPIIFSSLVVTFVIGNFANGFIALVNSIEWFKROKI-SFADQIITALAVS----- 54
      ||| : : : : : : : : : : : : : : : : : :
Db 41 FLPLPLYS-----LVFVPLGLGNSVVVLV-----LFKYKRLSRMTDVLNLNLAISDLLFVFL 92
      : : : : : : : : : : : : : : : : : :

QY 55 -----RVGLL-----WVLLNMYSTVLNPAFNSVEVRTTAYNIWAVINHFNSW 97
      : : : : : : : : : : : : : : : : : :
Db 93 PPMGYAARDQWVFLGLCKRMISWMLVGVFGIFFVWMLMSID-----RYLAIVHAVFSL 146
      : : : : : : : : : : : : : : : : : :

QY 98 LATTLSIFVLLKIANFSNFIPLHKRRVKSIVLVMLLGPLLPLACHLFLVNNNEIVRTKE 157
      ||| : : : : : : : : : : : : : : : : : :
Db 147 RARTLTYGVTSLATWSAVFASLP-----GFLFSTC--YTERNHTYCKTKY 191
      : : : : : : : : : : : : : : : : : :

QY 158 PEGNMTWKIKLSAMYFSNMVTVMVANLPFTLTLLSFMLICSL--CKHLKQWLHGKG 215
      : : : : : : : : : : : : : : : : : :
Db 192 SUNSTTWKV-----LSSLEINILGVLPLGLMFCYSMIRTLQHKNEKN----- 238
      : : : : : : : : : : : : : : : : : :

QY 216 SODPSTKVHIKALQTVISFLLC-----AIYFLSIMISVMSFGSLENKPVFMFC--- 264
      : : : : : : : : : : : : : : : : : :
Db 239 -----KAVKMIFAVVVLFLGFWTPNIVLPLETIVEL-----EVLQDCTPE 279
      : : : : : : : : : : : : : : : : : :

QY 265 -----KAIRFSYPSIHPIILWGNKKLKQTFSLV 294
      : : : : : : : : : : : : : : : : : :
Db 280 RYLDVAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQLF 319

RESULT 12
US-11-188-298-12382
; Sequence 12382, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298

Query Match 7.3%; Score 116; DB 6; Length 346;
Best Local Similarity 20.5%; Pred. No. 0.012;
Matches 63; Conservative 73; Mismatches 124; Indels 48; Gaps 15;

; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 12382
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-188-298-12382

Query Match 7.3%; Score 116.5; DB 7; Length 316;
Best Local Similarity 21.1%; Pred. No. 0.0099;
Matches 45; Conservative 39; Mismatches 66; Indels 63; Gaps 8;

QY 150 NEIVRTKEFEGNMTWKIKLSAMYFSNMVTVMVANLP-----FTLTLLSFML----- 197
      : : : : : : : : : : : : : : : : : :
Db 53 NDKILAGYVRETLSSWKKCLYSLFYWNNTNIVTLVPAIVYFVFAITLTNYFLIPVPPS 112
      : : : : : : : : : : : : : : : : : :

QY 198 -----LICSCLKKQWLHGKSGDPSQSTKVHIKALQTVISFLLC 238
      : : : : : : : : : : : : : : : : : :
Db 113 TMSDYTVINIFLWGAFLSCMLCSCFHC--MKQHSKQSNFWSKLDYLGIIISLCSMIP 170
      : : : : : : : : : : : : : : : : : :

QY 239 AIYF-LSIMISVMSFGSLENKPVFMFCAL-----RPSYPSIHP---FILING----- 282
      : : : : : : : : : : : : : : : : : :
Db 171 IYFGYFDHISYFSLFTIVTLVLTCTCVLHDKFNISTFRPRAMFFILFGSGLLPL 230
      : : : : : : : : : : : : : : : : : :

QY 283 -----NKKLKQTFSLVFWQMYVWVG 303
      : : : : : : : : : : : : : : : : : :
Db 231 TTGFFKFGIGVLNRIKVSF--VFWRALFYISG 261
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RESULT 13
US-10-455-772-442
; Sequence 442, Application US/10455772
; Publication No. US20060084054A1
; GENERAL INFORMATION:
; APPLICANT: John Alsobrook et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-589C
; CURRENT APPLICATION NUMBER: US/10/455,772
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/385615
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/402268
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/387606
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/386357
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/385755
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/386355
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/385490
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/420718
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/386447
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/386465
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1540
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 442
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-455-772-442

Query Match 7.3%; Score 116; DB 6; Length 346;
Best Local Similarity 20.5%; Pred. No. 0.012;
Matches 63; Conservative 73; Mismatches 124; Indels 48; Gaps 15;
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Search completed: April 27, 2006, 21:22:43  
Job time : 44 secs

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Db 930 ATGGTATATTTCTGCTCATCATTTTATCAATTTCTGGTAGTGTGTGGCATTTGTTCTTTGGA 989
Qy 61 AATTTTGTATAGGCTTCATAGCATCTGGTAATTCATTTAGTGTTCAGAGAGACAAAG 120
Db 990 AATTTTCCAATGGCTTCATAGCTCTAGTAATGTCAATTTAGTGTTCAGAGAGACAAAG 1049
Qy 121 ATCTCTCTTGTGACCAATTTCTACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 1050 ATCTCTCTGACCAATTCCTACTGCTCTGGGGTCTCCAGAAATTTGTTTACTCTGG 1109
Qy 181 GTATTATTATTAACCTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 1110 GTCATATTATTACATTTGGTATGCAATGTGTTTAAATCAGCTTTATATAGTTCAGAAGTA 1169
Qy 241 AGAAGTACTGCTTATTAATCTGGGAGTGAATCAACATTTTCCAGCACTGGCTTGTCTACT 300
Db 1170 GGAGCTGTGCTTCTAATATCTCAGCAATAATCAACCAATTTTCCAGCATCTGGCTGTCT 1229
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCCAACTTTATTTTCTTCAC 360
Db 1230 AGCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCCAACTTTATTTTCTTCAC 1289
Qy 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGTGTGATGTTGTTGGGGCTTTTGTCTATTTTG 420
Db 1290 CTAAGAGAGAGATTAGGAGTGTGTTCTGGTGATCTGTTGGTCCCTTGGTATTTTG 1349
Qy 421 GCTTGTCTATCTTTTGTGATAAATGAATGAGATTGTCGGGACAAAGAAATTTGAAGA 480
Db 1350 ATTGTGAATCTTGTCTGTATAACCATGAGTGTGTCGGGACAAAGAAATTTGAAGA 1409
Qy 481 ACATGACTTGTGAGATCAAAATGAGAGTGAATGTAATTTTCAATATGACTCTTAACC 540
Db 1410 AATGTGACTTGTGAAGATCAAAATGAGGAATGCAATACACCTTTCAAACTTTGACTGTAGC 1469
Qy 541 ATGTGTAGCAAACTTAGTACCTTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGT 600
Db 1470 ACATAGCAAACTCATACCTTTCATTTCTGACCTAATATGTTTCTGCTGTTAATCTGT 1529
Qy 601 TCTTTGTGTAACATCTCAAGAGATGCAAGCTCCATGTTGTAAGGATCTCAAGATCCAGC 660
Db 1530 TCTGTGATAAATCTCAAGAGATGCAAGCTCCATGTTGTAAGGATCTCAAGATCTCAGC 1589
Qy 661 ACCAAGTCCACATAAAGCTTTGCAAGCTGTGATCTCTCTCTGTTATGTGCTCAT 720
Db 1590 ACCAAGTCCACATAAAGCTTTGCAAGCTGTGATCTCTCTCTGTTATGTGCTCAT 1649
Qy 721 TACTTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAGTCTCGGAAACAAACCTGTC 780
Db 1650 TACTTTCTGTATCTTAATCACATTAACCTGGAATCTTTGAAACACAGAGACAAACTTGA 1709
Qy 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTCTGATCCATCCACCCATTCATCTGAT 840
Db 1710 TTCCTGCTTTGGCAACTCTTGGAACTCATGTATCTCTTCACTCACTCATCTCTGAT 1769
Qy 841 TGGGGAACACAGAAGCTAAAGCAGACTTTTCTTCAAGTTTGTGCAATAGGTAAGTGG 900
Db 1770 ATGGGAGCAGGAAGCTAAACAGAGCTTTCTTCAAGTTTATGTCAGTTCATGCTTA 1829
Qy 901 GTGAAGGAGAGAAGACTTTCATCTCCATAG 930
Db 1830 GTGAAGGAGACGACCCCTCACTCCATAG 1859
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RESULT 2
BZ604233/c
LOCUS WHADD117f Human MCF7 breast cancer cell line library (MCF7.1) Homo
DEFINITION sapiens genomic clone MCF7_1-19B22, genomic survey sequence.
ACCESSION BZ604233
VERSION BZ604233.1 GI:31512695
KEYWORDS GSS.
SOURCE Homo sapiens (human)
. ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
1 (bases 1 to 699)  
Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q.,  
Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P.,  
Gray, J.W. and Collins, C.  
End-sequence profiling: Sequence-based analysis of aberrant genomes  
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)  
12788976

CONTACT: Volik SV  
Colin Collins' lab  
UCSF Comprehensive Cancer Center  
UCSF Box 0808, San Francisco, CA 94143-0808, USA  
Tel: 415 502 7066  
Fax: 415 502 5665  
Email: svolik@cc.ucsf.edu  
This clone is available from Amplicon Express  
http://www.genomex.com

CLASS: BAC ends.  
LOCATION/Qualifiers  
1..699  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="MCF7\_1-19B22"  
/sex="female"  
/clone\_lib="Human MCF7 breast cancer cell line library (MCF7.1)"  
/note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN  
Query Match 72.5%; Score 674.6; DB 9; Length 699;  
Best Local Similarity 99.4%; Pred. No. 3.4e-167;  
Matches 677; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ATGATAACTTTTCAACCATCATTTTCCAGTCTGGTAGTGTACATTTGTTATGGA 60  
DB 681 ATGATAACTTTTCAACCATCATTTTCCAGTCTGGTAGTGTACATTTGTTATGGA 622  
QY 61 AATTTTGTATAGGCTTCATAGCATCTGGTAATTCATTTAGTGTTCAGAGACAAAG 120  
DB 621 AATTTTGTATAGGCTTCATAGCATCTGGTAATTCATTTAGTGTTCAGAGACAAAG 562  
QY 121 ATCTCTCTTGTGACCAAAATTTCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180  
DB 561 ATCTCTCTTGTGACCAAAATTTCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 502  
QY 181 GTATTATTATTAACTGGTATTCACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240  
DB 501 GTATTATTATTAACTGGTATTCACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 442  
QY 241 AGAAGTACTGCTTATAATATCTGGCAGTGAATCAACCACTTTCCAGCACTGGCTTGTACT 300  
DB 441 AGAAGTACTGCTTATAATATCTGGCAGTGAATCAACCACTTTCCAGCACTGGCTTGTACT 382  
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTTCTCCAACTTTATTTTCTTCAC 360  
DB 381 ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTTCTCCAACTTTATTTTCTTCAC 322  
QY 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTAGTGTGTGGGGCTTTGCTATTTTG 420  
DB 321 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTAGTGTGTGGGGCTTTGCTATTTTG 262  
QY 421 GCTTGTCTATCTTTTGTGATAAATGAATGAGATTGTCGGGACAAAGAAATTTGAAGA 480  
DB 261 GCTTGTCTATCTTTTGTGATAAATGAATGAGATTGTCGGGACAAAGAAATTTGAAGA 202  
QY 481 AACATGACTTGAAGATCAAAATTTGAAGAGTGAATGTAATTTTCAAAATAGTCTGAACC 540

Db 201 AACATGACTTGGAGATCAAAATGGAAGTGCATGACTTCTTCAAAATATGACTGTGAACC 142

Qy 541 ATGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTTTTAACTGT 600

Db 141 ATGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTTTTAACTGT 82

Qy 601 TCTTTGTGTAACATCTCAAGAAATGAGTGCAGTCCATGTTAAAGGATCTCAAGATCCCGAC 660

Db 81 TCTTTGTGTAACATCTCAAGAAATGAGTGCAGTCCGTTGTTAAAGGATCTCAAGATCCCGAC 22

Qy 661 ACCAAGGTCCACATAAAGCT 681

Db 21 ACGAAGTCCACATAAAGCT 1

RESULT 3

CO959975/c

LOCUS

DEFINITION

AGENCOURT\_30842526 NIH\_MGC\_145 Homo sapiens cDNA clone

IMAGE:7389866 3', mRNA sequence.

CO959975

CO959975.1 GI:51324548

EST.

Homosapiens (human)

ORGANISM

Homosapiens

REFERENCE

1 (bases 1 to 790)

NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: IRB18 row: h column: 12

High quality sequence start: 28

High quality sequence stop: 600.

High quality sequence stop: 600.

FEATURES

source

1. .790

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:7389866"

/tissue\_type="mixed"

/lab\_hosts="DH10B"

/clone\_lib="NIH\_MGC\_145"

/notes="vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmiI/XhoI-3', 5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at [http://image.llnl.gov/image/rearrayed\\_plates/IRB1.presv.dat](http://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat)

a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 49.5%; Score 460.6; DB 7; Length 790;

Best Local Similarity 80.8%; Pred. No. 1.5e-110;

Matches 572; Conservative 0; Mismatches 132; Indels 4; Gaps 3;

Qy 196 TGGTATTCACTGTTGTAATCCAGCTTTTAAATAGTGTAGAGTAAGAACTACTGCTTAT 255

Db 745 TGGTATGCAACTGTGTTAAATTC--TGCTTTTATATGGTTAGAAAGTAAGAA--TGTGCTTTNT 689

Qy 256 AATATCTGGGAGTGTATCAACCAATTTTCAAGCACTGGCTTGTACTTACCTCAGCATATTT 315

Db 688 AATCGNTGGGCTGTAAACCAATTTTCAAGCACTGGGCTGTACTTACCTCAGCATATTT 630

Qy 316 TATTGCTCAAGATGCAATTTCTCCAACTTTTATTTTCTTCACTTAAAGAGAGATT 375

Db 629 TGTGTTGCTCAAGATGCAATTTCTCCAACTTTTATTTCTCTCCACTTAAAGAGAAAT 570

Qy 376 AAGAGTGTCTTCTGTTGATGTTGTTGGGCTTTTGTATTTTGGCTTGTATCTTTT 435

Db 569 AAGAGTGTGTTCTGTTGATGTTGTTGGGCTTTTGGTATTTTCTGTTTGTATCTTGTCT 510

Qy 436 GTGATAAACATGAATGAGATTGTGGGCAACAAAGAAATTTGAAGGAAACATGACTTTGGAAG 495

Db 509 GTGATAAACATGAGAGAGTGTGGACAAAGAAATATGAAGGAAATGTGACTTTGGAAG 450

Qy 496 ATCAAAATGAAGAGTGCATGTTTCTTCAAAATATGACTGTAAACATGTTAGCAAACTTA 555

Db 449 ATCAAAATGAAGAGTGCATGTTTCTTCAAGCTTGTGACTGTAACTTCTAGCAAACTTC 390

Qy 556 GTACCCCTTCACTCTGACCTTACTTCTTATGTTTATGTTTATGTTTCTTCTTGTGTAACAT 615

Db 389 ATACCCCTTCTCTGAGCTTAATGTTTCTGCTGTTAATGTTTCTTCTTGTGTAACAT 330

Qy 616 CTCAAGAGATGCACTCCATGTTGTAAGGATCTCAAGATCCCAAGTCCCAACATGTTGTAACAT 675

Db 329 CTCAAGAGATGCGCTCCATGCAAGGATCTCAAGATCCCAAGTCCCAACATGTTGTAACAT 270

Qy 676 AAGCTTTGCAAACTGTGATCTCTCTCTGTTGTTATGTTGCAATTTACTTCTGTGCAATA 735

Db 269 AAGCTTTGCAAACTGTGATCTCTCTCTGTTGTTATGTTGCAATTTACTTCTGTGTAATA 210

Qy 736 ATGATATCAGTTGAGTTTGGAGTCTGGAAGTCTGGAAGCAAACTGTTCTGTTGTAACAT 795

Db 209 ATCAATCAACTGTTGAGTCTTAGGACACAGAGCAAACTTGTACTCTGTTGTAACAT 150

Qy 796 GCTATTAGATTCAGTATCTTCAATCCACCAATTCATCTGATTTGGGGAACAAAGAG 855

Db 149 ACTGTTGCAATGATCTCTTCAATCCCACTTCTGATTTATGTTGGAAGTAGGAAG 90

Qy 856 CTAAAGCAGACTTTCTTCTGATTTTGGCAAAATGAGGTACTGGGTG 903

Db 89 CTAAAGCAGACTTTCTTCTGATTTTGGGAGATGACACGCTGAGCG 42

RESULT 4

DN997644

LOCUS

DEFINITION

TC102961 Human breast cancer tissue, large insert, pcMV expression library Homo sapiens cDNA clone TC102961 5', similar to Homo sapiens similar to candidate taste receptor T2RP9 (LOC160669), mRNA sequence.

DN997644

DN997644.1 GI:66257471

EST.

KEYWORDS

SOURCE

ORGANISM

Homosapiens (human)

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 569)

Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L., Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts

Unpublished (2005)

Contact: Kovacs, KF

High Throughput cDNA Cloning

Origene Technologies, Inc. ( [www.origene.com](http://www.origene.com) )

6 Taft Court, Suite 100, Rockville, MD 20850, USA

Tel: 301 340 3188  
Fax: 301 340 8606  
Email: cdna@origene.com

This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.  
Please contact Origene for access.

Origene Technologies, Inc.  
6 Taft Ct. Suite 100  
Rockville, MD 20850

Tel: (301) 340-3188

http://www.origene.com

Seq primer: pCMV6 5prime forward vector primer, Origene Technologies Inc.

Location/Qualifiers

1..569

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="TC102961"

/tissue\_type="Breast cancer"

/clone\_lib="Human breast cancer tissue, large insert, pCMV expression library"

/note="Organ: Mammary gland (cancer tissue); Vector:

pCMV6-XL5; Site 1: EcoRI; Site 2: XhoI/Sall compatible end

ligatio; Oligo-dT primed reverse transcription optimized

for large and GC rich mRNA transcripts, cDNA size

selection, optimized ligation for large inserts into

mammalian expression vector, random clones selected for

end sequence verification of full-length genes"

## ORIGIN

Query Match 40.6%; Score 378; DB 8; Length 569;

Best Local Similarity 94.0%; Pred. No. 1e-88;

Matches 393; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 ATGATAAATCTTTCTACCCCATCATTTTTCAGTCTGTAGTGGTTACATTTTGTATTGGA 60

Db 152 ATGATAAATCTTTCTGCCCATCATATTTCCATCTAGTAGTGGTTACATTTGTATTGGA 211

Qy 61 AATTTGCTAAATGGCTTCATAGACATGGTAAATTCATTTAGTGGTTCAGAGACAAAAG 120

Db 212 AATTTGCTAAATGGCTTCATAGCGTTGGTAAATTCACCGAGTGGTGAAGACAAAAG 271

Qy 121 ATCTCCTTTGCTGACCAATTTCTACTGCTCTGGGGTCTCCAGAGTGGTTCCTCGG 180

Db 272 ATCTCCTTTGCTGACCAAAATTTGCTACTGCTCTGGGGTCTCCAGAGTGGTTCCTCGG 331

Qy 181 GTATTATTATTAACCTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240

Db 332 GTGTTATTATTAATTTGGTATTCAACTGTGTTGAATCCAGCTTTTGTAGTGTAGATTGA 391

Qy 241 AGAATCTACTGCTATAATATCTGGGAGTGTATCAACCATTTTCCAGCACTGGCTTGTACT 300

Db 392 AGAATCTACTGCTATAATATCTGGGAGTGTATCAACCATTTTCCAGCACTGGCTTGTACT 451

Qy 301 ACCCTCAGCATATTTATTGCTCAGATTGCCAATTTCTCCAACTTTATTATTTTCTTAC 360

Db 452 AGCCTCAGCATATTTATTGCTCAGATTGCCAATTTCTCCAACTTTATTATTTTCTTAC 511

Qy 361 TTAAGAGAGAGAGTTAAGAGTGTCAATTCGTGATGTTGTTGGGGCTTTTGTCTATTTT 418

Db 512 TTAAGAGAGAGAGTTAAGAGTGTCAATTCGTGATGTTGTTGGGGCTTTTGTCTATTTT 569

## RESULT 5

DQ040209

LOCUS

DEFINITION

Qy

Accession

Version

Keywords

Source

DQ040209 Homo sapiens TAS2R14 gene, 954 bp DNA linear GSS 02-JUN-2005

Genomic survey sequence.

DQ040209 Virtual Transcription, partial sequence,

DQ040209.1 GI:66991418

GSS.

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 954)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,

White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and

Chimpanzees

(er) PLOS Biol. 3 (6), E170 (2005)

15869325

2 (bases 1 to 954)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,

White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment. Translation starts at the beginning of

alignment.

Location/Qualifiers

1..954

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="12"

<1..>954

/gene="TAS2R14"

/locus\_tag="HC6720"

## ORIGIN

Query Match 36.6%; Score 340.8; DB 11; Length 954;

Best Local Similarity 63.6%; Pred. No. 8e-79;

Matches 589; Conservative 0; Mismatches 322; Indels 15; Gaps 4;

Qy 9 TTTTCTACCCATCATTTTTCAGTCTGGTGTGTTTACATTTTGTATTGGAAATTTTGC 68

Db 9 TGTCTAAGAGCATATTTTACATTCGTTTTTAATGTGGAAATTTAATTTGGAATTTAGG 68

Qy 69 TAATGGCTTCATAGACATGGTAAATTCATTTAGTGGTTCAGAGACAAAAGATCTCCTT 128

Db 69 AAATAGTTTCATAGACATGGTAAATTCATTTAGTGGTTCAGAGACAAAAGATCTCCTT 128

Qy 129 TGCTGACCAATTTCTACTGCTCTGGGGTCTCCAGAGTGGTTCCTGGGTATTATT 188

Db 129 GGTTCATCGGATCTCTACTGCTTTGGCAATCTCTCGAATTAGCCTGGTTGGTTAATAT 188

Qy 189 ATTAACCTGGTATTTCACACTGTGTTCAATCCAGCT--TTTAATAGTGTAGAAGTAAGAAC 245

Db 189 CGGAAGCTGGTGTGTCTGTGTTTTTCCAGCTTTATTTGCCACTGAATAATGTTCTAG 248

Qy 246 TACTGCTTATATATCTGGGAGTGTATCAACCATTTTCAGCACTGGCTTGTCTACCTCT 305

Db 249 AATGCTTACTAATATCTGACAGTGTATCAATCATTTTGTGTCTGGTTAGCTACAGGCT 308

Qy 306 CAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAATTTTATTTTCTTCACTTAA 365

Db 309 CGGTACTTTTATTTTCTCAAGATAGCCAAATTTTCTAACTATTTTCTTCTACCTAAA 368

Qy 366 GAGGAGAGTTAAGAGTGTCTCTGATGTGTGTGGGGCTTTTGTCTATTTTGTGCTTG 425

Db 369 GTGGAGGGTTAAAGAGTGGTGTGTGTGCTCTCTGTGACTTCGGTCTCTGTTTTT 428

Qy 426 TCATCTTTTGTGATAAATGAAATGAGATTGCGGACAAAGAAATTTTGAAGGAAACAT 485

Db 429 AAATATTGCACTGATAAATGAAATGAGATTGCGGACAAAGAAATTTTGAAGGAAACAA 488

Qy 486 GACTTGGAGATCAATTTGAAGAGTGCATGTACTTTTCAATATATGACTGTGTA----AC 539

Db 489 GACTTGGAGATCAATTTGAAGAGTGCATGTACTTTTCAATATATGACTGTGTA----AC 548

540	Qy	CATGGTAGCAAACTTAGTACCCCTTCACTCTGACCTACTATCTTTTATGCTGTTTAATCTG	599
549	Db	CACGTGTGTTCAATTTTATACACCTTTACTTTGTGCTCGCAATGTTTCTTCTCCTCATCTTT	608
600	Qy	TTCTTTTGTGTAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAAG	659
609	Db	CTCCATGTGGAAACATCCGAAGAAGATGCAGACACTGTCAAAATATCCGGAGAGCCGAG	668
660	Qy	CACCAAGTCCACATPAAAGACTTTTGCAACTGTGATCTCCTTCTCTTGTATTGTGCCAT	719
669	Db	CACCAAGCCCCACAGAGGAG--TTTAAAGTGTGATCACTTTTCTTCTACTCTATGCCAT	725
720	Qy	TTACTTTCTGTGCCATAATGATATCAGTTTGTGGAGTTTTTGGAGCTGTGGAAAAACAACCTGT	779
726	Db	TTTCTCTCTGTCTTTTTTTCATATCAGTTTGGACCTCTGAAAGGTTGGAGGAAAA--TCT	782
780	Qy	CTTCATGTTCTTGCAAGACTATTAGATTACGCTATCCTTCAATCCACCCATTCATCCTGAT	839
783	Db	AAATTATTCTTTTCCCAGGTGATGGGAATGGCTTATCCTTCATGCTCACTCAATGTTTCTGAT	842
840	Qy	TTGGGGAACAAGAGCTTAAAGCAGACTTTTCTTTTCAGTTTTTTTGGCAAAATCAGGTTACTG	899
843	Db	TCTTTGGAACAAGAAGCTCAGACAGCCCTCTCTGTCAAGTGCTACTCTGTGCGCTGAGGTACAT	902
900	Qy	GGTGAAGGAGAGAAGACTTTCATCTC	925
903	Db	GTTTCAAGATGGGGAGCCCTCAGGTTC	928

RESULT 6	AL037695	554 bp	linear	EST 04-SEP-2003
LOCUS	AL037695			
DEFINITION	DRFZP56400672.r1 564 (synonym: hfr2) Homo sapiens CDNA clone			
	DKFZP56400672.5, mRNA sequence.			
ACCESSION	AL037695			
VERSION	AL037695.3	GI:5928268		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Homnidae; Homo.			
REFERENCE	1 (bases 1 to 554)			
AUTHORS	Blum, H., Bauersachs, S., Mewes, H.W., Gaassenhuber, J. and Wiemann, S.			
TITLE	EST (Blum, et al.)			
JOURNAL	Unpublished (1999)			
COMMENT	On Jul 7, 1999 this sequence version replaced gi:5866546.			

## ORIGIN

Query Match	36.2%	Score 336.8	DB 1	Length 554	
Best Local Similarity	81.5%	Pred. No. 8e-78			
Matches 427	Conservative	0	Mismatches 92	Indels 5	Gaps 3
QY	21	CAATTTTTCAGTCTCGGTAGTGGTTACATTTGTTTATTGGAAATTTTCTTAATGGCTTCAT	80		
DB	4	CAATTTATCAATTCCTGGTAGTGGTTGCAATTTGTTCTTGGAATGTTGCCAATGGCTTCAT	63		
QY	81	AGCACTGGTAAATTCATTCAGTGGTTCAAGAGACAAAAGATCTCTTTTCTGACCAAAAT	140		
DB	64	AGCTCTAGTTAAATGCTCAATGACTGGGTTAAGACACAAAAGATCTCTCAATGACCAAAAT	123		
QY	141	TCTCAGTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTATTATTAACCTGGTA	200		
DB	124	TGTCAGTCTCTGGCAATCTCCAGAAATGGTTTACT-TTGATCATATTATTACATGGTA	182		
QY	201	TTCAACTGTGTGAATCCAGCTTTTAATAGTGTAGAGTAAGAACTACTGCTTATAATAT	260		
DB	183	TGCMACTGTGTAAATTCAGCTTTATATAGTTTGAAGTAAGAATGTTCTCTCTAATGT	243		
QY	261	CTGGGCACTGATCAACCAATTTTCAGCACTGGCTTGCTACTACCTCAGCATATTTTATTT	320		
DB	243	CTGGGCAATTAATCAATCAATTCAGCAATTTGGCTTGCTACGAGCTCAGCATATTTTATTT	302		
QY	321	GCTCAAGATTGCCAATTTCTCCAACTTATTTTCTTCACTTAAAGAGGAGGATTAAAG	380		
DB	303	GTTCAAGATTGCCAATTTCTCCAAATTTTATTTTCTCCACTAAAGAGAGAAATTAAG	362		
QY	381	TGTCATTTCTGTGATGTTGTTGGGCGCTTGTGCTATTTTGGCTTGTCATCTTTTGTGAT	440		
DB	363	TGTTCTCTTGTGATCTGTTGGGCTCCTTGGTATTTTGAATTTGTAATCTTCTGTGTT	422		
QY	441	AAACAT--GAATGAGATTGTCGGACAAAAGAAATTTGAAGGAAACATGACTTGG--AAGA	496		
DB	423	AACATGGGATGACAGGTGTGTCGACAAAAGAAATTTGAAGGAAATGACTTGGGAAGGA	482		
QY	497	TCAATTTGAAGAGTGCAATGACTTTTCAAAATGACTGTAAAC	540		
DB	483	TCGAATTTGAGGAATGCAATACACCTTTCAAAACATGACTATAACC	526		
RESULT 7					
CE692204/c					
LOCUS	tigr-gss-dog-17000368584316	DNA	500 bp	linear	GSS 29-SEP-2003
DEFINITION	genomic survey sequence.				Dog Library Canis familiaris genomic,
ACCESSION	CE692204				
VERSION	CE692204.1	GI:37011274			
KEYWORDS	GSS.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	1 (bases 1 to 500)				
AUTHORS	Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.				
TITLE	The dog genome: survey sequencing and comparative analysis				
JOURNAL	Science 301 (5641), 1898-1903 (2003)				
PUBMED	14512627				
COMMENT	Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: ekirknes@tigr.org Class: shotgun.				
FEATURES	Location/Qualifiers				
source	1..500				
	/organism="Canis familiaris"				
	/mol type="genomic DNA"				

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/organism="Canis familiaris"
/mol type="genomic DNA"

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/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 32.8%; Score 304.8; DB 10; Length 500;
Best Local Similarity 75.6%; Pred. No. 2.3e-69;
Matches 378; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

Qy 189 ATTAACCTGTTTCAACCTGTTGAATCCACGCTTTTAATAGCTAGAGTAAGAATAC 248
Db 500 AATAAATGTTATGCACTCTGTTGAATCCACGCTTTTAATAGCTAGAGTAAGAATAC 441

Qy 249 TCGTTATATATCTGGCAGTGCATCAACCAATTCAGCACTGGCTTGTCTACTACCTCAG 308
Db 440 TGTTCATATTCCTGACAGCAGCAATCATTTTAGCATCTGGCTTGTCTACTAGCTCAG 381

Qy 309 CATATTTATTTGCTCAAGATTCGCAATTTCTCCAACTTTATTTCTTCACTTAAGAG 368
Db 380 TGTATTTTATTTGTTCAAAATAGCAATTTCTTAACCTTATTTTCTCGCCTAAGTG 321

Qy 369 GAGAGTTAAGAGTGTCTCTGCTGATGTTGTTGGGCTTTGCTATTTTGGCTTGTCA 428
Db 320 GAGAGTTAAGAGTGTCTCTGCTGATGTTGTTGGGCTTTGCTATTTTGGCTTGTCA 261

Qy 429 TCTTTTGTGATAACATGAATGAGATTTGTCGGAACAAAGAAATTTGAAGGAAACATGAC 488
Db 260 TGTTCGAATGTTAAGCGTATATGAGCAATGCAATGAGGAATATGAAGGAAACATGAC 201

Qy 489 TTGGAAGATCAAAATGAGAGTGCATGTACTTTTCAATATGACTGTAAACCATGGTAGC 548
Db 200 TAGGCAGACCAAACTGAGGACATTTGCACAGCTTATGAATATGACTGTATTCACGCTAAT 141

Qy 549 AAATCTAGTACCTCTCACCTCTACTCTTTTATGCTGTTAACTGTTCTTTTGG 608
Db 140 GAATCTTGTACCTTGTCTATATCTTTAATCATCTTTTGTCTGTTTAACTTTTCCCTGTG 81

Qy 609 TAAACATCTCAAGAGATGACGCTCCATGGTAAAGATCTCAAGATCCAGCACCAGGT 668
Db 80 GAAACATCTCAAGAGATGAGATCCAGTGGTAAAGATCCCAAGTTCAGCACCAGGT 21

Qy 669 CCACATAAAGCTTTGCCAA 688
Db 20 CCACATAAAGCGCATGCAGA 1

RESULT 8
DQ040210
LOCUS
DEFINITION
DQ040210
Pan troglodytes TAS2R14 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
DQ040210
VERSION
DQ040210.1 GI:66891419
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE
1 (bases 1 to 796)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
Chimpanzee
(er) PLoS Biol. 3 (6), E170 (2005)
15869325
2 (bases 1 to 796)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
```

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Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
Location/Qualifiers
source
1..796
/organism="Pan troglodytes"
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/locus_tag="HC6720"

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Query Match 31.7%; Score 294.8; DB 11; Length 796;
Best Local Similarity 64.0%; Pred. No. 1.1e-66;
Matches 497; Conservative 0; Mismatches 267; Indels 12; Gaps 3;

Qy 9 TTTTCTACCCATCAATTTTCCAGTCTGGTGTGTTACATTTGTTATTTGGAATTTGCG 68
Db 9 TGTCTATAAGAGCATATTTACATTCGTTTAAATTTGTGGAATTTATATTTGGAATTTAGG 68

Qy 69 TAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGACACAAAAGATCTCCTT 128
Db 69 AATATAGTTTCATAGCACTGGGGAATGTTATGACTGGGTCAAGGGAAGAAATCTCTTC 128

Qy 129 TGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTCTGGTATTAT 188
Db 129 AGTTGATCGGATCCTCACTGCTTTGGCAATCTCTAAATTTAGCGTTGGTTTAAATAT 188

Qy 189 ATTAACTGGTATTCAACTGTGTTGAATCCAGCT---TTTAAATAGTGTAGAGTAAGAAC 245
Db 189 CGGAAGCTGGTGTGTCTGTGTTTTCAGCTTTTATTTGCACTGAAAATAATGTTTCAG 248

Qy 246 TACTGCTTATATATCTGGGAGTATCAACCATTTTCAGCACTGGCTTGTCTACTACCT 305
Db 249 AATGCTTACTAATATCTGGACAGTATCAATCATTTTGTCTGTTGTAGCTACAGGCT 308

Qy 306 CAGCATATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTATTTTCTTCACTTAAA 365
Db 309 CGGTACTTTTATTTTCTCAAGATAGCCAAATTTTCTAACTCTATTTTCTCTACTAAA 368

Qy 366 GAGGAGATTAAAGTGTCTCTGGTGTATGTTGTGGGCTTTGTCTATTTTGGCTTG 425
Db 369 ATGGAGAGTTAAAAGGTTGGTTTGGTGTCTGCTTCTGTGACTTCCGGTCTTCTCTTTT 428

Qy 426 TCATCTTTTGTGATAAAACATGAATGAGATTTGTGGGACAAAAGAAATTTGAAGGAAACAT 485
Db 429 AATATTTGCACTGATAAACATCCATATATAATGCCAGTATCAATGGATACAGAAACAA 488

Qy 486 GACTTGGAGATCAAAATGGAAGAGTGCATGTTTTCATTTTCAAATATGACTGTGTA-----AC 539
Db 489 GACTTGCAGTCTCTGATTCAAGTAACCTTTACACGATTTTCCAGTCTTATTTGATTAACCCAG 548

Qy 540 CATGTTGCAAACTTAGTACCTTTCACCTCTGACCTTACTATCTTTTATGCTGTTAATCTG 599
Db 549 CACTGTGTCTATTTTTCATACCTTTTACCTTTGTGTCCTGGCAATGTTTCTTCTCTCATCTT 608

Qy 600 TTCTTTGTGTAACATCTCAAGAAAGTGCAGTCTCATGTTAAAGGATCTCAAGATCCCCAG 659
Db 609 CTCCATGTGGAACATCCGAAAGAGATGCAGACACTGTCAAAAAGATCCGGAGAGCCAG 668

Qy 660 CACCAAGTGCACATAAAAGCTTTTGCAAAATGTTGATCTCTCTTCTCTTGTGTATGCGCAT 719
Db 669 CACCAAGGCCACAGAGGAG---TTAAAGATGATGATGACTTTTCTTCTCTACTCTATGCCAT 725

Qy 720 TTACTTTCTGTCCATAATGATATCATCTAGTTTGGAGTTTTCGAACTCTGGAACAAAC 775
Db 726 TTTCTCTCTGTCTTTTTCATATCATGTTTGGACCTCTGAAAGGTTGGAGGAAATC 781
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RESULT 9
AQ164951/c
LOCUS
DEFINITION
  HS_3014 B2 H07 MR CIT Approved Human Genomic Sperm Library D Homo
  sapiens genomic clone Plate=3014 Col=14 Row=P, genomic survey
  sequence.
ACCESSION
  AQ164951.1 GI:3563146
VERSION
  GSS.
KEYWORDS
  SOURCE
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 397)
REFERENCE
  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
  Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  10449764
COMMENT
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Sequence tagged Connector
  Plate: 3014 row: P column: 14
  Class: BAC ends
  High quality sequence stop: 397.
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    /sex="male"
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    E-Coli DH10B"
ORIGIN
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  Best Local Similarity 83.6%; Pred. No. 2e-66; Indels 0; Gaps 0;
  Matches 332; Conservative 0; Mismatches 65;
  Qy 353 TTCTTCACTTAAAGAGGAGGTTAAGAGTGTCAATCTCGTGATGTTGTGGGGCCTTTGC 412
  Db 397 TTCATCACTTANAAGGAAGGCTAAGAGTGTAGTTCTCGTGATAGTGTGGGCTTTGT 338
  Qy 413 TATTTTGGCTGTGCATCTTTTGTGATAAATGATGATGTTGTGGGACAAAGAAT 472
  Db 337 TCTTTTGGTTGTCAACTGTGTGATGAAACACACGTATATAAATGTGTGGACAGAAGAT 278
  Qy 473 TTGAAGGAAACATGACTTTGGAGATCAATTTGAAGTGCAATGTTTTCATATAGA 532
  Db 277 GTGAAGGAAACGTAACCTTTGGAAGATCAAACTGAGGATGCAATGACCTTTTCAACTTGA 218
  Qy 533 CTGTAACCATGGTAGCAAACTTAGTACCTTCACTCTGACCTCACTATCTTTTATGCTGT 592
  Db 217 CTGTAGCCATGCTAGCAAACTTGATACCACTTCACTCTGACCTGATATCTTTCTGCTGT 158
  Qy 593 TAATCTGTTTGTGTAAACATCTCAAGAGATGCAATGATGTTGTTGAAGATCTCAAG 652
  Db 157 TAATCTACTCTGTGTAAACATCTCAAGAGATGCAATGATGTTGTTGAAGATCTCAAG 98
  Qy 653 ATCCAGACCAAGGTCACATAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTAT 712
  Db 97 ATCCAGACCAAGATCCACATAAAGCTTGTCAAACTGTGACCTCTTCTCTGATATAC 38

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Qy 713 GTGCCATTACTTTCTGTCCATAATGATATCAAGTGTGAGTTTGGAGTCTGGAAACA 772
Db 37 TTGCCATTACTTTCTGTGTCTTAATCATATCTCTTTG 1
RESULT 10
B17827
LOCUS
DEFINITION
  B17827.TPB CIT978SKA1 Homo sapiens genomic clone A-347L19, genomic
  survey sequence.
ACCESSION
  B17827
VERSION
  B17827.1 GI:2125576
KEYWORDS
  SOURCE
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 466)
REFERENCE
  Adams,M.D., Kelley,J.M., Rounsley,S.R. and Venter,J.C.
  Use of a BAC End Sequence Database for Sequence-Ready Map Building
  Unpublished (1997)
  Other_GSSs: 347L19.TVB
  Contact: Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: mdadams@tigr.org
  Clones are available from Research Genetics (info@resgen.com). BAC
  end search page:
  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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  Class: BAC ends.
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  Best Local Similarity 82.2%; Pred. No. 5.7e-64;
  Matches 327; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
  Qy 533 CTGTAAACCATGGTAGCAAACTTAGTACCTTCACTCTGACCTCACTATCTTTTATGCTGT 592
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  Qy 593 TAATCTGTTCTTTGTGTAAACATCTCAAGAGATGCAATGATGTTGAAGATCTCAAG 652
  Db 61 TAATCTGTTCTTTGTGTAAACATCTCAAGAGATGCGGCTCCATGAGCAAGATCTCAAG 120
  Qy 653 ATCCAGACCAAGGTCACATAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTAT 712
  Db 121 ATCCAGACCAAGGTCACATAAAGCTTTGCAAACTGTGACCTCTTCTCTCATGTTAT 180
  Qy 713 GTGCCATTACTTTCTGTCCATAATGATATCAAGTGTGAGTTTGGAGTCTGGAAACA 772
  Db 181 TTGCCATTACTTTCTGTGTATAATCAATCAACTTGGAACTTAGGACACAGCAGACA 240
  Qy 773 AACCTGTCTTCTATGTTCTGCAAAAGCTATTAGATTCAGCTATCTTCAATCCACCATTTCA 832
  Db 241 AACTTGTACTCTGCTTTGCCAACTGTGCAATCATGATCTTCACTTCCACTCATTTCA 300
  Qy 833 TCCTGATTTGGGAAACAAGAGCTTAAAGCAGACACTTTTCTTTCAGTCTTTTGGCAAATGA 892

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||||| 301 TCTGATATGGAAGTAGGAGCTAAACACAGCCTTCTTTCAGTTTGTGGCAGATGA 360  
||||| 893 GGTACTGGGTGAAAGAGAGAGACTTCATCTCCATAG 930  
||||| 361 CATGCTGAGTGAAGAGAGAGAAACCTCAACTCCATAG 398

RESULT 11  
CR071716/c  
LOCUS  
DEFINITION  
Forward strand read from insert in 5'HPRT insertion targeting and  
chromosome engineering clone MHPN99102, genomic survey sequence.  
CR071716  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.  
1 (bases 1 to 870)  
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,  
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,  
Rogers, J., and Bradley, A.  
Direct Submission  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICER  
Location/Qualifiers  
1. .870  
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Query Match 29.7%; Score 276.6; DB 11; Length 870;  
Best Local Similarity 59.6%; Pred. No. 7.6e-62;  
Matches 506; Conservative 0; Mismatches 334; Indels 9; Gaps 2;  
QY 43 GTTACATTTGTTATTTGGAATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTGAG 102  
DB 870 GTGGAATTAGTAATTGGAATTATAGGAATGGTTTCATGCTGCTCCACTGTATGGAC 811  
QY 103 TGGTTCAAGAGACAAAGATCTCTTTGCTGACCAAAATTCCTCAGCTCTCGGGGTCTCC 162  
DB 810 TGGGTTAAGAAAAGAAAATGCTCCCTAGTTAATCAAAATTCCTACTGCTTTGTCAATCTCC 751  
QY 163 AGAGTTGGTTGCTCTGGGTATTATTATTAATCACTGTTTGAATCCAGCT 222  
DB 750 AGAATTTTTCAGCTCTGTTATTGTTTAAAGTTAGTAATCAACTTTTCATATACAGAT 691  
QY 223 TT---TAATAGTGTGAAGTGAAGAACTACTGCTTATAATATCTGGCAGTGTACCAACAT 279  
DB 690 TTAACACAGTTCAGGATGATACAGTCATGACAACTGCTGGATTTAGCCACCAT 631  
QY 280 TTCAGCAACTGGCTTCTACTACCTCAGCATATTTTATTGCTCAAGATTGCCAATTC 339  
DB 630 TTCAGCATCTGGATTCTCATGCTCTCACTGCTCTTATTATTCTTAAAGATAGCAATTTT 571  
QY 340 TCCAACTTTATTTTCTTCACTTAAGAGAGAGTTAAGAGTCTCATCTCTGTTGATGTTG 399  
DB 570 TCTAACTCTTTTCTTTCTTATCTAAAGTGAGAGTTGAAAAGTAGTTTCAGTTACACTG 511  
QY 400 TTGGGGCCTTTGCTATTTTGGCTTCTCATCTTTTGTGATAAAACATGAATGAGATTGTG 459  
DB 510 TTGGTGTCTATGCTCTCTCTGATTATTTAAATATTTTACTAACTTAACTTGAACCGACATG 451  
QY 460 CGGACAAAAGATTTGAAGAAACATGACTTGGAGATCAATTTGAAGAGTGAATGTAC 519  
DB 450 TGGACAAATGAATATCAAGAAACATATATGACGCTTCAGTTCTCATTTACTATGCAAG 391

QY 520 TTTTCAAATATGACTGTAA-----CCATGGTAGCAAACTTAGTACCTTCACTCTGACC 573  
DB 330 TGTACAGGAGGTGTTAAGGCTTCACATATTTTCTGTCTGTCCCGCTTTTGTGTC 331  
QY 574 CTACTATCTTTTATGCTGTTAATCTGTTCTTTTGTGTAAACATCTCAAGAAATGACAGTTC 633  
DB 330 CTGTCAACTTTTCTCTGCTCATCTCTCTCCCTGTGGACACATCAACAAGAGGATGACGAC 271  
QY 634 CATGTAAGGATCTCAAGATCCAGACCAAGGTCACATATAAAGCTTTGCAAACTGTG 693  
DB 270 CATGTTCCAGGAGGAGAGATGCCAAGACCAAGGCTTCACAAAGCCCTACAAACTGTG 211  
QY 694 ATCTCTCTCTCTGTTATGTCCTTACTTTTCTGTCATATGATATGATATGATTTGGAGT 753  
DB 210 ATTGCAATTTTCTCTACTATATTCATTTTATCTGCTGCTTATATACAAATTTGGAAA 151  
QY 754 TTTGGAAGTCTGGAAAAACAACTCTCTTCATGTTCTGCAAGCTATTAGATTCAGTAT 813  
DB 150 TATGAATTTACTGAAGAAAAATCTTTTCGTTGTTATTTGTGAGGTTGTATATATAGCTTT 91  
QY 814 CTTCAATCCACCATTCTGATTTGGGGAACAGAACTAAAGCAGACTTTTCTT 873  
DB 90 CGACATCTCCATTCATATATTTCTGATTGTAGGAGACATGAAGCTGAGACAGGCTGCCTG 31  
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DB 30 CTTCTCTGT 22

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LOCUS  
DEFINITION  
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mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
BG402330  
BG402330.1 GI:13295778  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 677)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Cloned through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM1334 row: n column: 03  
High quality sequence stop: 636.  
Location/Qualifiers  
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FEATURES  
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sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGCGGCGGCACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones



and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

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ORIGIN
Query Match      28.8%; Score 267.6; DB 2; Length 677;
Best Local Similarity 92.1%; Pred. No. 1.7e-59;
Matches 293; Conservative 0; Mismatches 24; Indels 1; Gaps 1;
QY 613 CATCTCAAGAAGATCAGCTCCATCGGTAAAGGATCTCAAGATCCAGACCAAGTCCAC 672
Db 1 CATCTCAAGAAGATCAGCTCCATCGCAAGGATCTCAAGATCCAGACCAAGTCCAC 60
QY 673 ATAAAGCTTTGCAAACTGTGATCTCTTCCTCTTGTGTTATGTCATTTCTGTGCC 732
Db 61 ATAAAGCTTTGCAAACTGTGATCTCTTCCTCTTGTGTTATGTCATTTCTGTGCC 120
QY 733 ATATGATATCAGTTTGGAGTTTGGAGTCTGGAAACCAACCTGCTCTCATGTTCTGC 792
Db 121 ATGATCATATCAGTTTGTAAATTTTGGAGGCTGGAAAGCAACCTGCTCTCATGTTCTGC 180
QY 793 AAAGCTATTAGATTAGCTATCTTCAATCCACCCATTCATCTGATTTGGGAAACAAG 852
Db 181 CAGCTATTATTCAGCTATCTTCAACCCACCATTCATCTGATTTGGGAAACAAG 240
QY 853 AAGCTAAAGCAGACTTTCTTTCAGTTTGGGCAATGAGGTACTGGGTGAAGAGAG 912
Db 241 AAGCTAAAGCAGATTTTCTTTCAGTTTGGGCAATGAGGTACTGGGTGAAA-GACAG 299
QY 913 AAGCTTTCATCTCCATAG 930
Db 300 AAGCTTTCGCTCCATAG 317
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LOCUS DQ040211 Homo sapiens TAS2R13 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION DQ040211
VERSION DQ040211.1 GI:66891420
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (ex) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 761)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Best Local Similarity 62.2%; Pred. No. 1.6e-56;
Matches 458; Conservative 0; Mismatches 266; Indels 12; Gaps 3;
QY 152 TGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTAATTAATAACCTGGTATTAACCTGTGT 211
Db 1 TGGCAATCTCCAGAAATGGGCTGATCTGGGAAATATTAGTAAGTTGGTTTGGTCTCTGC 60
QY 212 TGAATCCAGCT--TTTAATAGTGTAGAAGTAAGAATCTGCTTATATATCTGGCAG 268
Db 61 ATTATCTAGCCATATTTGTGCTGGAACAGGAATTAAGAATTAATGATTTTGTAGTGAATAG 120
QY 269 TGATCAACCATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATTTTATTTTGGTCAAGA 328
Db 121 TTTCTAATCATCTCAATCTCTGGCTTGCTACAATCTTCAGCATCTTTTATTTTGTCTCAAAA 180
QY 329 TTGCCAATTTCTCCAACTTTATTTTCTTCTTAAAGAGGAGAGTTAAGAGTGTCAATTC 388
Db 181 TAGCGAGTTTCTTAGCCCTGCTTTCTTCTATTTTGAAGTGGAGAGTAACAACAAAGTGATTC 240
QY 389 TGGTGATCTGTTGGGGCTTTGCTATTTTGGCTTGTTCATCTTTTGTGATAAATCATCA 448
Db 241 TGATGATCTGCTAGGAACCTTTGGTCTTCTTATTTTAAATCTGATACAAATAAATCATGC 300
QY 449 ATGAGATTGTGGCGCAAAAGAAATTTGAAGGAAACATGACTTTGGAGAGATCAAAATGAAGA 508
Db 301 ATATAAAGAGCTGGCTGGACCGATATGAAGAAACACAACCTTGGAAATTCAGTATGAGTG 360
QY 509 GTGCAATGTACTTTTCAAAATATGACTGTAAACATGGTAGCAAACTT-----AGTACCCT 562
Db 361 ACTTTGAAACATTTTTCAGTGTGGTCAAAATTCACATGATGTTTCACTTCAATCAACCAT 420
QY 563 TCACCTTGACCTTACTATCTTTTATGCTGTTTAACTGTTCTTTTGTGATAAATCTCAAGA 622
Db 421 TTACTGTGGCTTTCATCTCTTTTCTCCTGTTAAATTTTCTCCTGTCAGAAACATCTCCAGA 480
QY 623 AGATGCAGCTCCATGGTAAAGATCTCAAGATCCCAGACCAAGGTCCACATAAAAGCTT 682
Db 481 AAATGCACTCAATTTACAAGGACACAGAGACCCAGCCAGCCAGGTCCATACAAATGCT 540
QY 683 TGCAAACTGTGATCTCTTCTTCTTGTATGTCATTTTGTGTCATTTCTGTCATTAATGATAT 742
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QY 743 CAGTTTGGAGTTTGGAGTCTGGAAACAAACCTGTTCTTCTATGTTCTGCAAGCTATTTA 802
Db 601 CA---TGGATTTCTGAGCTGTATCAGACACAGATGATCTACATGCTTTTGTGAGACGATTG 657
QY 803 GATTGAGTATCTCTTCAATCCACCCATTCATCTGATTTGGGGAACCAAGAGCTAAAGC 862
Db 658 GAGTCTTCTCTCTTCAAGCCACTCTTCTTCTGATTTCTAGGAACCGCTAAGTTAAGAC 717
QY 863 AGACTTTTCTTTCAGT 878
Db 718 AGGCCTTTCTTTTGGT 733
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RESULT 14
LOCUS AW266498 ZG24 gastric epithelial cell GES-1 Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION AW266498
VERSION AW266498.1 GI:6646676
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 330)
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AUTHORS	Zhao, J.R., Yan, X.J., Han, F.C., Cui, D.X., Hou, Y., Yan, Q.J. and Su, C.Z.
TITLE	Gastric associated differentially expressed gene mRNA sequence
JOURNAL	Unpublished (1999)
COMMENT	Contact: Zhao JR Institute of Genetic Diagnosis, the Fourth Military Medical University Xi'an, China, 710032 Tel: 86 029 3374771 Email: Zhaojr@263.net Seq primer: M13 Forward POLVA=Yes.

FEATURES	source
Location/Qualifiers	
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/note="differentially expressed gene sequences from human gastric epithelial cell GES-1. The method used is DDRT-PCR. The control cell line is human gastric carcinoma cell Gc7901"	

ORIGIN	Query Match	Score	DB 1;	Length
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Qy	531	GACTGTACCACTGGTAGCAAACTTAGTACCTTCACCTCTGACCCCTACTATCTTTTATGCT	590
Db	2	GACTGTAAACCATGCTAGCAAACTTAGTACCTTCACCTCTGATTAACCTGATCTTTCTCTGCT	61
Qy	591	GTTAACTCTGTTCTTTTGTGTAAACATCTCAAGAAATGCAGCTCCATGGTAAAGGATCTCA	650
Db	62	GTTAGTCTGTTCTCTGTGTAAACATCTCAAGAAATGCACCTCCATGGCAAAAGGATCTCA	121
Qy	651	AGATCCCAAGCACCAGGTCACATAAAGCTTTTGCAAACTGTGATCTCCTTCTCTTGTT	710
Db	122	AGATCCCAAGTACCAGGTCACATAAAGTTTTCGAAACTGTGATCTCCTTCTCTTGTT	181
Qy	711	ATGTGCCATTACTTTCTGTGCCAATGATATC-AGTTTGGAGTTTTTGGAAAGCTGGAAA	769
Db	182	ATGTGCCATTACTTTGTGTCTGTAATAATATCAAGTTTGGAGTTTTTGAAGATCTGGAAA	241
Qy	770	ACAAACCTGTCCTCATGTTCTTGCAAGCTATTAGATTCACTATCCTTCAATCCACCCAT	829
Db	242	ACAAACCTGTCCTCATGTTCTTGCAAGCTATTGGATTCACTGTTCTTCAGCCCAACCGT	301
Qy	830	TCATCCTGA	838
Db	302	TCATCCTGA	310

RESULT 15					
CO926496					
LOCUS	CO926496	711 bp	mRNA	linear	EST 16-AUG-2004
DEFINITION	AGENCOURT 30488268 NIH MGC 145 Homo sapiens				cdna clone
	IMAGE:7211789 5'				mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
C0926495				
C0926496.1	GI:51281173	EST.	Homo sapiens (human)	
			Homo sapiens	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRB15 row: a column: 03  
High quality sequence stop: 549.

a note: this is a minusc library.

ORIGIN	Query Match	26.7%;	Score 248;	DB 7;	Length 711;
	Best Local Similarity	63.7%;	Pred.No. 2.7e-54;		
	Matches 412;	Conservative 0;	Mismatches 226;	Indels 9;	Gaps 2;
QY	9	TTTTCTACCCATCAATTTTTCCAGTCCTGCTAGTGGTTACATTTGTTATTGGAATTTTGC	68		
Db	64	TGTCATAAAGAGCATATTACATTCGTTTAAATGTGGAAATTTATATTGGAATTTTAGG	123		
QY	69	TAAATGGCTTCATAGCACTGGTAAATTCATGTAGTGGTTCAAGAGACAAAGAATCTCCCTT	128		
Db	124	AAATAGTTTCATAGCACTGGTGAACGTGATAGCTGGTCAAGGAAGAAGATCTCTTC	183		
QY	129	TGCTGACCAAAATCTCACTGCTCTGGCGGCTCCAGAGTTGGTTGCTCTGGGTATATT	188		
Db	184	GGTTGATCGATCCTCACTGCTTTGGCAATCTCTCGAATTAGCCTGGTTGGTTAATATT	243		
QY	189	ATTAAACTGGTATTCAACTGTGTGAATCCAGCT---TTTAATAGTGTAGAAGTGAAGAC	245		
Db	244	CGGAAGCTGGTGTGTCTGTGTTTTTCCAGCTTTATTTCGCCACTGAAAAAATGTTCCAG	303		
QY	246	TACTGCTTATAATATCTGGGCAGTGAATCAACCATTTTCAGCAACTGGCTTGCTACTACCCCT	305		
Db	304	AATGCTTACTAATACTCGACAGTGATCAATCATTTTAGTGTCTGTTAGCTACAGGCCT	363		
QY	306	CAGCATATTTTATTTGCTCAAGATTCGCCAATTTCTCCAACCTTATTTTCTTCACATTAAA	365		
Db	364	CGGTACTTTTTTATTTTCTCAAGATAGCCAATTTTCTAACTCTATTATTTTCTCTACCTAAA	423		
QY	366	GAGGAGAGTTAAGAGTGTCAATCTGTGTGATGTTGTTGGGCGCTTGTCTATTTTGGCTTG	425		
Db	424	GTGGAGAGTTAAAGAAGTGGTTTTGGTGTCTGCTTCTGTGCACTTCGGTCTTCTTGTTTTT	483		
QY	426	TCATCTTTTTTGTGATAAAATGAATGAGATGTGCGGACAAAGAAATTTGAAGGAACAT	485		
Db	484	AAATATTGCACATGATAAATCCATATAAATGCCAGTATCAATGGGATACAGAAGAAACAA	543		
QY	486	GACTTGGAGATCAAAATTTGAAGGTGCAATGTACTTTTCAATAATGACTGTA-----AC	539		
Db	544	GACTTCGAGTTCGATTCNAGTAACCTTTACAGATTTTCCAGTCTTATTGTATTAACACG	603		
QY	540	CATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTTATGCTGTTAATCTG	599		

Db 604 CACTGTGTTTCATTTTCATACCCCTTTACTTTGTCCCTGGCAATGTTTCTCTCCTCATCTT 663  
Qy 600 TTCTTTGTGTAACATCTCAAGAAGATGCAGCTCCCATGGTAAAGGAT 646  
Db 664 CTC CATGTGGAAACATCGCAGAAGATGCAGCACACTGTCTCAAAATAT 710

Search completed: May 1, 2006, 08:16:01  
Job time : 4558 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2006, 20:16:31 ; Search time 312 Seconds  
(without alignments)  
5298.501 Million cell updates/sec

Title: US-09-825-882-7

Perfect score: 930

Sequence: 1 atgataacttttaccat.....agaagacttcattccatag 930

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/ina/1/COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5/COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A/COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B/COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H/COMB.seq.\*
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- 8: /cgn2\_6/ptodata/1/ina/RE/COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827.6	89.0	250352	3	US-09-949-016-14724
2	684.4	73.6	903	3	US-09-393-634-63
C 3	536.6	57.7	601	3	US-09-949-016-108237
C 4	530.6	57.1	601	3	US-09-949-016-108296
C 5	481.4	51.8	601	3	US-09-949-016-108297
C 6	472.2	50.8	601	3	US-09-949-016-108236
C 7	451.2	48.5	601	3	US-09-949-016-108441
C 8	449.4	48.1	601	3	US-09-949-016-108442
C 9	428.4	46.1	601	3	US-09-949-016-108480
C 10	424.4	45.6	601	3	US-09-949-016-108328
C 11	406	43.7	601	3	US-09-949-016-108440
C 12	404.4	43.5	601	3	US-09-949-016-108327
C 13	398.6	42.9	601	3	US-09-949-016-108134
C 14	379	40.8	601	3	US-09-949-016-108139
C 15	368.8	39.7	601	3	US-09-949-016-108443
C 16	347.6	37.4	601	3	US-09-949-016-108273
C 17	345.6	37.2	601	3	US-09-949-016-108326
18	340.8	36.6	954	3	US-09-393-634-61
C 19	336.8	36.2	554	3	US-09-393-634-67
C 20	331.2	35.6	601	3	US-09-949-016-108438
C 21	308.2	33.1	912	3	US-09-393-634-59
C 22	295.6	31.8	601	3	US-09-949-016-108481
C 23	293.6	31.6	397	3	US-09-393-634-73
C 24	288.2	31.0	391	3	US-09-949-016-108349

C 25	286.6	30.8	500	3	US-09-949-016-108350	Sequence 108350,
C 26	284.4	30.6	466	3	US-09-393-634-71	Sequence 71, Appl
C 27	281.6	30.3	601	3	US-09-949-016-108329	Sequence 108329,
C 28	277.4	29.8	601	3	US-09-949-016-108366	Sequence 108366,
C 29	269.6	29.0	601	3	US-09-949-016-108272	Sequence 108272,
C 30	241.2	25.9	601	3	US-09-949-016-108367	Sequence 108367,
C 31	226.4	24.3	2438	3	US-09-393-634-4	Sequence 4, Appl
C 32	220	23.7	954	3	US-09-949-016-3382	Sequence 3382, Ap
C 33	220	23.7	957	3	US-09-949-016-15124	Sequence 15124, A
C 34	220	23.7	924	3	US-09-393-634-54	Sequence 54, Appl
C 35	207	22.3	924	3	US-09-393-634-52	Sequence 52, Appl
C 36	205	22.0	939	3	US-09-393-634-50	Sequence 50, Appl
C 37	192	20.6	930	3	US-09-393-634-20	Sequence 20, Appl
C 38	186.8	20.1	1084	3	US-09-393-634-18	Sequence 18, Appl
C 39	181.8	19.5	1532	3	US-09-949-016-108437	Sequence 108437,
C 40	179.6	19.3	601	3	US-09-393-634-16	Sequence 16, Appl
C 41	178.6	19.2	1739	3	US-09-393-634-8	Sequence 8, Appl
C 42	175.4	18.9	1540	3	US-09-393-634-40	Sequence 40, Appl
C 43	172.4	18.5	951	3	US-09-949-016-2336	Sequence 2336, Ap
C 44	172.4	18.5	951	3	US-09-949-016-14078	Sequence 14078, A
C 45	172.4	18.5	4951	3	US-09-949-016-14078	Sequence 14078, A

## ALIGNMENTS

### RESULT 1

US-09-949-016-14724  
; Sequence 14724, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14724  
; LENGTH: 250352  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(250352)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14724

Query Match 89.0%; Score 827.6; DB 3; Length 250352;

Best Local Similarity 93.1%; Pred. No. 9e-226;

Matches 866; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy	1	ATGATACTTTTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTGTTATTGGA 60
Db	122572	ATGATACTTTTCCGCCATCATTTTCCATTTAATAGTGGTTACATTGTTATTGGA 122631
Qy	61	AATTTCTTAATGGCTTCATGACACTGTAATTCATTGAGTGGTTCAAGACAAAAG 120
Db	1226..2	AATTTCTTAATGGCTTCATGACACTGTAATTCATTGAGTGGTTCAAGACAAAAG 122691
Qy	121	ATCTCTTTGTCACAAAATTCACAGTCTCTGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db	12269?	ATCTCTTTGTCACAAAATTCACAGTCTCTGCGGTCTCCAGAGTTGGTTGCTCTGG 122751
Qy	181	GTATTATATTAACCTGGTATTCACTGTGTTGAATCCAGCTTTTAAATAGTGTAGTAAGTA 240

Db 122752 GTATTAGTATTAAATGGTATGCAACTGAGTTGAATCCAGCTTTTAAACAGTATAGAAGTA 122811  
Qy 241 AGAACTACTGCTTAAATATCTGGGAGTATCAACCAATTCAGCAACTGGCTTCTACT 300  
Db 122812 AGAATTACTGCTTAAATATCTGGGAGTATCAACCAATTCAGCAACTGGCTTCTACT 122871  
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCAACTTTTATTTTCTTCAAC 360  
Db 122872 AGCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCAACTTTTATTTTCTTCAAC 122931  
Qy 361 TTAAGAGAGAGAGTTAAGAGTGTCAATCTGGTGATGTTTGTGGGCCCTTTTGTCTATTTTG 420  
Db 122932 TTAAGAGAGAGAGTTAAGAGTGTCTTCTGGTGATGTTTGTGGGCCCTTTTGTCTATTTTG 122991  
Qy 421 GCTTGTCACTTTTGTGATTAACATGAATGAGATTGCGGACAAAGAAATTTGAAGGA 480  
Db 122992 GTTGTGCATCTTTTGTGATTAACATGAATGAGATTGCGGACAAAGAAATTTGAAGGA 123051  
Qy 481 AACATGACTTGAAGATCAAAATGGAAGAGTGAATGTAATTTTCAAAATATGACTGTAAACC 540  
Db 123052 AACATGACTTGAAGATCAAAATGGAAGAGTGAATGTAATTTTCAAAATATGACTGTAAACC 123111  
Qy 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGT 600  
Db 123112 ATCCTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTCTGCTGTTAATCTGT 123171  
Qy 601 TCTTTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCAGC 660  
Db 123172 TCTCTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCAGC 123231  
Qy 661 ACCAAGGTCCATAAAGCTTTGCAAACTGTGATCTCCTCTCTGTTATGTGCCATT 720  
Db 123232 ATGAAGGTCCATAAAGCTTTGCAAACTGTGATCTCCTCTCTGTTATGTGCCATT 123291  
Qy 721 TACTTTCTGTCATATGATATGATGAGTTTGGAGTTTGGAGTCTGGAAAAACAAACCTGTC 780  
Db 123292 TACTTTCTGTCATATGATATGATGAGTTTGGAGTCTGGAAAAACAAACCTGTC 123351  
Qy 781 TTCATGTTCTGCAAGCTATTAGATTGATGATGATGATGATGATGATGATGATGATGATGAT 840  
Db 123352 TTCATGTTCTGCAAGCTATTGATGATGATGATGATGATGATGATGATGATGATGAT 123411  
Qy 841 TGGGGAACAAAGAGCTAAGCAGACTTTTCTTTCAGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTT 900  
Db 123412 TGGGGAACAAAGAGCTAAGCAGACTTTTCTTTCAGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTT 123471  
Qy 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930  
Db 123472 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 123501

## RESULT 2

US-09-393-634-63  
; Sequence 63, Application US/09393634  
; Patent No. 6558910

## GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Ryba, Nick  
; APPLICANT: Mueller, Ken  
; APPLICANT: Hoon, Mark  
; APPLICANT: The Regents of the University of California  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
; FILE REFERENCE: 02307E-098000US  
; CURRENT APPLICATION NUMBER: US/09/393,634  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 63  
; LENGTH: 903

; TYPE: D1/2  
; ORGANISM: Homo sapiens  
; FEATURE  
; OTHER INFORMATION: human GR15  
US-09-393-634-63

Query Match 73.6%; Score 684.4; DB 3; Length 903;  
Best Local Similarity 85.7%; Pred. No. 7, 4e-186;  
Matches 773; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

Qy 1 ATGATAACTTTTTCACCCATCATTTTTCAGTCTGGTAGTGGTTTACATTTGTTTATGGA 60  
Db 1 ATGATAACTTTTTCACCCATCATTTTTCAGTCTGGTAGTGGTTTACATTTGTTTATGGA 60  
Qy 61 AATTTTGTCTAATGCGTTTCATAGCAGTGTAAATTCATTTGAGTTTCAAGAGACAAAAG 120  
Db 61 AATTTTGTCTAATGCGTTTCATAGTGTAAATTCATTTGAGTTTCAAGAGACAAAAG 120  
Qy 121 ATCTCCTTTTGTGACCAAAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180  
Db 121 ATCTCCTTTTGTGACCAAAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180  
Qy 181 GTATTATTATTAACCTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240  
Db 181 GTATTATTATTAACCTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240  
Qy 241 AGAATCTGCTTATAATATCTGGGAGTGTATCAACCAATTTTCAGCAACTGGCTTGTCTACT 300  
Db 241 AGAATCTGCTTATAATATCTGGGAGTGTATCAACCAATTTTCAGCAACTGGCTTGTCTACT 300  
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCAAAATTTCTCAACTTTTATTTTCTTCAAC 360  
Db 301 AGCCTCAGCATATTTTATTTGCTCAAGATTGCAAAATTTCTCAACTTTTATTTTCTTCAAC 360  
Qy 361 TTAAGAGAGAGAGTTAAGAGTGTCAATCTGGTGATGTTTGTGGGCCCTTTTGTCTATTTTG 420  
Db 361 TTAAGAGAGAGAGTTAAGAGTGTCAATCTGGTGATGTTTGTGGGCCCTTTTGTCTATTTTG 420  
Qy 421 GCTTGTCACTTTTGTGATTAACATGAATGAGTTTGGGAGTGTGGGACAAAAGAAATTTCAAGA 480  
Db 421 GTTGTGTCATCTTGTGTGGTAAACATGATGAGAGTATGTGGGACAAAAGAAATTTCAAGA 480  
Qy 481 AACATGACTTGGAAAGATCAAAATTTGAAGAGTGTCAATGTATCTTTTCAAAATATGACTGTAAACC 540  
Db 481 AACATGACTTGGGAGATCAAAATTTGAGTGTATCCGAGCCACTTTTCAAGATATGACTGTAAACC 540  
Qy 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGT 600  
Db 541 ACGCTTGCAGAACTTAAATACCCCTTTTACTCTGCTCCCTGTTTATCTTTTCTGCTTAAATCTGT 600  
Qy 601 TCTTTTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCAGC 660  
Db 601 TCTTTTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCAGC 660  
Qy 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCAATT 720  
Db 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCAATT 720  
Qy 721 TACTTTCTGTCATATGATATGATGAGTTTGGAGTTTGGAGTCTGGAAAAACAAACCT 777  
Db 721 TACTTTCTGTCATATGATATGATGAGTTTGGAGTTTGGAGTCTGGAAAAACAAACCT 780  
Qy 778 GTCCTTCATGTTCTGCAAGCTATTAGATTGATGATGATGATGATGATGATGATGATGATGATGAT 837  
Db 781 GTCTCTCATGCTCAGCAAAAGCTTCACTCAATATATATATATATATATATATATATATATATATAT 840  
Qy 838 ATTTGGGGAACAAAGAGCTAAGAGTAAAGCAGACTTTTCTTTCAGTTTTCAGTTTTCAGTTTTCAGTT 897  
Db 841 ATTTGGGGAACAAAGAGCTAAGAGTAAAGCAGACTTTTCTTTCAGTTTTCAGTTTTCAGTTTTCAGTT 900  
Qy 898 TG 899  
Db 901 TG 902



Db 1 C 1

## RESULT 5

US-09-949-016-108297/c  
; Sequence 108297, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 108297  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-108297

Query Match 51.8%; Score 481.4; DB 3; Length 601;  
Best Local Similarity 92.2%; Pred. No. 8.5e-128;  
Matches 506; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

Qy 382 GTCAATTCGGTGATGTTGTGGGCGCTTTGCTATTTTGGCTGTGCATCTTTTGTGATA 441  
Db GTTGTCTGGTGATACTATGGGCGCTTTGCTATTTTGGTTGTGATCTTTTGTGATA 542

Qy 442 AACATGATGAGATTGTCGGHCAAAAGAAATTTGAAGAAACATGACTTGGAGATCAA 501  
Db AACATGAATCAGATTATATGGAACAAAGAAATTAAGAGAAACATGACTTGGAGATCAA 482

Qy 502 TTGAAGAGTGCAATGACTTTTCAATATGACTGTAAACCATGGTAGCAAACTTAGTACC 561  
Db CTGAGAGTGCAATGACTTTTCAATATGACTGTAAACCATGGTAGCAAACTTAGTACC 422

Qy 562 TTCACCTGACCCCTACTATCTTTTATGCTGTTAAATCTGTTTGTGTAACATCTCAAG 621  
Db TTCACCTGACCCCTGATACTCTTCTGCTGTTAAATCTGTTTGTGTAACATCTCAAA 362

Qy 622 AGATGCGAGCTCCATGGTAAAGGATCTCAAGATCCAGACCAAGGTCCACATAAAGCT 681  
Db AAGATGCGAGCTCCATGGCAAGGATCTCAAGATCCAGATCCAGATCCACATAAAGCT 302

Qy 682 TTGCAAACTGTGATCTCTCTCTCTGTTATGTGCAATTTACTTTCTGTCCATAATGATA 741  
Db WTGCAAACTGTGATCTCTCTCTCTGTTATGTGCAATTTACTTTCTGTCCATAATCATG 242

Qy 742 TCAGTTTGGAGTTTGGAGTCTGGAAGCTGGAAGCAAAACCTGTCTTCATGTTCTGCAAGCTATT 801  
Db TCAGTTTGGAGTTTGGAGTCTGGAAGCTGGAAGCAAAACCTGTCTTCATGTTCTGCGAAGCTATT 182

Qy 802 AGATTTCAGTATCTCTCAATCCACCCATTCATCTGATTTGGGGAACCAAGAGCTAAAG 861  
Db GCAATTTCAGTATCTCTCAATCCACCCATTCATCTGATTTGGGGAACCAAGAGCTAAAG 122

Qy 862 CAGACTTTTCTTTCAGTTTGTGGCAAAATGAGGTACTGGGTGAAAGGAGAGAACTTCA 921  
Db CAGACTTTTCTTTCAGTTTGTGGCATGTGAGGTACTGGGTGAAAGGAGAGAACTTCA 62

Qy 922 TCTCCATAG 930  
Db TCTTCATAG 53

## RESULT 6

US-09-949-016-108236/c  
; Sequence 108236, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 108236  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-108236

Query Match 50.8%; Score 472.2; DB 3; Length 601;  
Best Local Similarity 93.4%; Pred. No. 3.7e-125;  
Matches 492; Conservative 1; Mismatches 34; Indels 0; Gaps 0;

Qy 1 ATGATAACTTTTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60  
Db ATGATAACTTTTTCGCCCATCATATTTTCCATTTAGTAGTGGTTACATTTGTTATTGGA 468

Qy 61 AATTTTGTAAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAAG 120  
Db AATTTTGTAAATGGCTTCATAGCGTTGGTAAATTCACCGAGTGGTGAAGAGACAAAAG 408

Qy 121 ATCTCTTTGCTGACCAAAATTTCTACCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180  
Db ATCTCTTTGCTGACCAAAATTTGTCACTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 348

Qy 181 GTATTATTATTAAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240  
Db GTGTTATTATTAAATTTGGTATTCAACTGTGTTGAATCCAGCTTTTTRTAGTGTAGAATTA 288

Qy 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTGTACT 300  
Db AGAACTACTGCTTATAATATCTGGGCACTAACCAGGCAATTTTCAGCAACTGGCTTGTACT 228

Qy 301 ACCCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCAACTTTTATTTTCTTCAC 360  
Db AGCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCAACTTTTATTTTCTTCGC 168

Qy 361 TTAAGAGAGAGATTAAAGAGTGTCACTCTGGTGTGATGTTGTTGGGCGCTTTTGTATTTTTG 420  
Db TTAAGAGAGAGATTAAAGAGTGTCACTCTGGTGTGCTGTTGTTGGGCGCTTTTGTATTTTTG 108

Qy 421 GCTTGTCACTTTTGTGATAAAACATGAATGAGATGTGCGGACAAAAGAAATTTGAGGA 480  
Db GCTTGTCACTTTTGTGATAAAACATGAATGAGATGTGCGGACAAAAGAAATTTGAGGA 48

Qy 481 AACATGACTTCGAGATCAAAATTTGAAGAGTCAATGTACTTTTCAAA 527  
Db AACATGACTTCGAGATCAAAATTTGAAGAGTCAATGTACTTTTCAAA 1

## RESULT 7

US-09-949-016-108441/c  
; Sequence 108441, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.





; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 108480  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-108480

Query Match 46.1%; Score 428.4; DB 3; Length 601;  
Best Local Similarity 82.0%; Pred. No. 1.3e-112;  
Matches 492; Conservative 1; Mismatches 107; Indels 0; Gaps 0;  
QY 308 GCATATTTTATTTGCTCAAGATGCGCAATTTCTCCAACTTTATTTTCTTCACTTAAAGA 367  
DB 601 GCATATTTTATTTGCTCAAGATGCGCAATTTCTCCAACTTTCTTTTCTTCACTTAAAGA 542  
QY 368 GGAGAGTTAAGAGTGTCATTTCTGCTGATGTTGTTGGGCGCTTTGCTATTTTGGCTTGTGTC 427  
DB 541 GGAGAGTTAAGAGTGTCATTTCTGCTGATGTTGTTGGGCGCTTTGCTATTTTGGCTTGTGTC 482  
QY 428 ATCTTTTGTGATATAATGAATGAGATTTCTGGGCAAAAGAAATTTGAGGAAACATGA 487  
DB 481 ATCTTTTGTGGCAAAATGATGAGATTTCTGGGCAAAAGAAATTTGAGGAAACATGA 422  
QY 488 TTGGGAAGATCAAAATGCAAGATGCAATGTACTTTTCAATATGACGTAAACCATGCTAG 547  
DB 421 CTGGGAAGATGAAATGAGGAAATACGATACATCTTTTCATATTTGACGTAACTACCCAT 362  
QY 548 CAAACTTAGTACCTTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGTTCTTTGT 607  
DB 361 GGAGCTTCATACCTTTACTCTGCTGATATCTTTTCTGATGCTAATCTGTTCTCTGT 302  
QY 608 GTAACATCTCAAGAGATGAGCTCCATGTAAGATCTCAGATCCGACCCAGCAAGG 667  
DB 301 RTAAACATCTCAAGAGATGAGCTCCATGTAAGATGAGATGAGATGAGATGAGATGAG 242  
QY 668 TCACATAAAAGCTTTTGCACAACTGTGATCTCTTCTCTCTTGTATGTCATTTTACTTTTC 727  
DB 241 TCACATAAAAGCTTTTGCACAACTGTGATCTCTTCTCTCTTGTATGTCATTTTCTTTC 182  
QY 728 TGCCATAATGATATACGTTTGGAGTTTGGAGTCTGGAATGGAACAAACCTGCTTCAATGT 787  
DB 181 TATTCCTAATCGTTTCGTTTGGAGTCTTAGAGGCTGCGGAATGACCCGCTTGTCTATGG 122  
QY 788 TCTGCAAGCTATTAGATTGAGCTATCTTCAATCCACCCATTCATCTGATTTGGGGAA 847  
DB 121 TTAGCAAGCTGTTGGAAACATATATCTGCAATTCGACTCATCTCATCTAATTTGGAGAA 62  
QY 848 ACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGGCAAAATGAGGTACTGCGTGAAAG 907  
DB 61 CCAAGAGCTAAACACACCTTTCTTTTGTATTTTGTCTCAGATTAGTGTGCTGAGTAAAG 2

RESULT 10  
US-09-949-016-108328/c  
; Sequence 108328, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 108328  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-108328

Query Match 45.6%; Score 424.4; DB 3; Length 601;  
Best Local Similarity 82.7%; Pred. No. 1.8e-111;  
Matches 496; Conservative 1; Mismatches 102; Indels 1; Gaps 1;  
QY 145 ACTGCTCTGGGCTCTCCAGAGTTGGTTGCTCTGGGTATTTATTTAAACTGGTATCA 204  
DB 601 ACTGCTCTGGGCTCTCCAGAAATTTGTTACTCTGGGTCATATTTATTTCAATGGATGCA 542  
QY 205 ACTGTTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTATAATATCTGG 264  
DB 541 ACTGTTTGAATTTGGGTTTCATATAGATTAGAAGTAAGAAATTTTGGTCTTAATGCTCA 482  
QY 265 GCAGTGTCAACCAATTTTCCAGCACTGCTTACTACCTCAGCATATTTTATTTGCTC 324  
DB 481 GCAATAACCAAGCAATTTTCCAGCATCTGG-GTGTACTAGCTCAGCATATTTCAATTTGCTC 423  
QY 325 AAGATTGCCAATTTCTCCAACTTTATTTTCTTCACTTAAAGAGAGAGTTAAGAGTCTC 384  
DB 422 AAGACTGCCAATTTTCTCCAACTTTATTTTCTCACCCTAAAGAGAGAGTTAAGAAATGT 363  
QY 385 ATTCGTGTGATGTTGTTGGGCGCTTGTCTATTTTGGCTTGTCTCTTTTGTGATAAAC 444  
DB 362 GGTGTTGTTGATGCTGTTGGGCGCTTGTGATTTTTCATTTGTTATCTTGTCTCTGATAAC 303  
QY 445 ATGAATGAGATTTGTCGGACAAAAGAAATTTGAAGAAACATGACTTGAAGAGTCAAAATG 504  
DB 302 AYGGGTGAGAGTGTGTGGACAAAAGAAATTTGTCTGATGATCAAAATG 243  
QY 505 AAGAGTGCATGTACTTTTCAAAATATGACTGTACCATGTTAGCAAACTTAGTACCCCTC 564  
DB 242 AGGAATGCAATACAGCTTTTCAAACTGACTGTAACTGACCCAGCAAAAGCTCACACCTGTC 183  
QY 565 ACTCTGACCTTACTATCTTTTATCTGTTAATCTGTTCTTTTGTGTAAACATCTCAAGAAG 624  
DB 182 ACTCTGACATTAATCTTTTCTGCTGTTAATCTTCTCCATGTAAACATGTCAAGAAG 123  
QY 625 ATGAGTCCATGTAAGAGATCTCAAGATCCAGACCAAGGTCACATATAAAGCTTTG 684  
DB 122 ATGAGCTCCATGTAAGAGATCTCAACATCTCAGCACCAAGGTGCACATAAAGCTTTG 63  
QY 685 CAAACTGTGATCTCTCTCTCTTCTGTTATGTCGCAATTTACTTTTCTGTCATATGATATCA 744  
DB 62 CAAACTGTGATCTCTCTCTCTTATGTTATTTGCCATTTACTTTCTGTTCTATCATCATCA 3

RESULT 11  
US-09-949-016-108440/c  
; Sequence 108440, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 108440

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-108440

Query Match 43.7%; Score 406; DB 3; Length 601;

Best Local Similarity 82.7%; Pred. No. 3.3e-106;

Matches 463; Conservative 1; Mismatches 96; Indels 0; Gaps 0;

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2Y 1 ATGATAACTTTTCTACCCATCAATTTTCCAGTCGTGAGTGGTATCAATTTGTTATGGA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 561 ATGATGAGTTTCTACACATGTTTTTCCATCTAGTAGTGGTGTCAATTTATCTTGA 502
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 AATTTTGTCTAATGGCTTCATAGCACGTGTAATTTCCATTTAGTGGTTCAGAGACAAAAG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 501 AATTTTGGCAATGGCTTTATAGCACGTGTAATTTCAATTCCTGGGTCAAGAGACAAAAG 442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 ATCTCCTTTGCTGACCAAAATTCACCTGCTGCGCGGTCTCCAGAGTTGGTTGCTCTGG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 ATCTCCTGAGCTGATCAAAATTTATGCTGCTCTGCGAGTCTCCAGAGTTGGTTGCTCTGG 382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GTATTATTATTAACCTGATTCAACTGCTGTTGAATCCAGCTTTTAACTAGTAGAGTA 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 381 GTAATATTATTACATGGTATTCAACTGCTGTTGAATCCAACTTCATCTAATTTAAAGTA 322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 AGAATCTACTGCTTATAATATCTGGGAGTATCAACCAATTTCCAGCAACTGGCTTGCTACT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 321 ATAAATTTTATTCTAATGCTGCGGAGTAACCAATCAATTTCCAGCATCTGGCTTGCTACT 262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 ACCCTCAGCATATTTATTGCTCAAGATGCAATTTCTCCAACTTTATTTTCTTTCAC 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 AGCCTCAGCATATTTATTGCTCAAGATGCTCAATTTCTCCAGACTTATTTTTCATCAC 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 TTAAGAGGAGGTTAAGAGTGTCACTGCTGATGTTGTTGGGCTTTGCTATTTTTC 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 TTAAGAGGAGGCTAAGAGTGTGATGTTGTTGGTATAGTGTGGGCTTTGTTCTTTTG 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 GCTTGTCTATCTTTTGTGATAACATGAATGAGATGTGGGACAAAAGAAATTTGAAGGA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 GTTGTGACCTTGTGATGAACACACAGTATATAAATGTGGACAGAGATGTGAAGGA 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 ACATGACTTGAAGATCAAAATGAAGAGTGAATGCTATTTTCAATATGACTGTAAAC 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 AACGTAACCTTGAAGATCAAACTGAGGAATGCAATGCACCTTTCCAACTGACTGTAGCC 22
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 ATGCTAGCAAACTTAGTACC 560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 ATGCTAGCAAACTTAGTACC 2
```

RESULT 12

US-09-949-016-108327/c

; Sequence 108327, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 108327

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-108327

Query Match 43.5%; Score 404.4; DB 3; Length 601;

Best Local Similarity 81.7%; Pred. No. 9.6e-106;

Matches 490; Conservative 1; Mismatches 107; Indels 2; Gaps 2;

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QY 70 AATGGCTTCTATAGCACGTGTAATTTCCATTCAGTGGTTCAGAGACAAAAGATCTCCCTTT 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 600 AATGGCTTCTATAGCACGTGTAATTTCCATTCAGTGGTTCAGAGACAAAAGATCTCAACA 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 130 GCTGACCAAAA-TTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATATT 188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 540 GCTGACCAAAAATTTCTCACTGCTCTGGGTGTCAGAAATTTGGTTTACTCTGGGTCAATTT 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 189 ATTAAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAGTAAGAACTAC 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 ATTACATTTGGTATGCAACTGTGTTTAAATTTGGCTTCATATAGATTAGAAGTAAGAAATTTT 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 TGCTTATAATATCTGGGAGTGTATCAACCAATTTCCAGCAACTGGCTTGCTACTACCCTCAG 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 TGGTTCTAATGTCTCAGCAATAACCAAGCAATTTCCAGCATCTGG-GTGTACTAGCCTCAG 362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 CATATTTTATTTGCTCAAGATTTGCCAATTTCTCCAACTTTATTTTCTTCACTTAAAGAG 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CATATTTTCAATTTGCTCAAGACTGCCAATTTCTCCAACTTTATTTTCTCCACCTAAAGAA 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 GAGAGTTAAGAGTCTCACTCTGGTGATGTTGTTGGGCGCTTTGCTATTTTGGCTTGCA 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 RAGAAATTAAGAAATTTGGTTTGGTGATGCTGTTGGGCGCTTTGTTATTTTCAATTTGTAA 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 TCTTTTGTGATAAAACATGAATGAGATTTGTCGGGACAAAAGAAATTTGAAGGAAACATCAC 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 TCTTGTCTGATTAACCAAGCTGTGAGTGTGTGACAAAAGAAATTAAGGAAATTTGTC 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 489 TTGGAAGATCAAAATTAAGAGTGAATGTAATTTTCAAAATATGACTGTGAACATGTGTAGC 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TTGGATGATCAAAATTTGAGGAATGCAATACAGCTTTTCAAACTTTGACTGTGAACATGCCAGC 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 549 ARACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTTATCTCTTTCTTTG 608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 AAACGTCACACCTTGCACCTCTGACACTAAATCTTTTCTGCTGTAAATCTATTTCTCCATG 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 609 TAAACATCTCAAGAAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCAGCACCACCAAGGT 668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TAAACATGTCAAGAAGATGCAGCTCCATGGCAGGAAGGATCTCAACATCTCAGCACCACCAAGGT 2
```

RESULT 13

US-09-949-016-108134/c

; Sequence 108134, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 108134

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-108134

Query Match 42.9%; Score 398.6; DB 3; Length 601;  
Best Local Similarity 51.2%; Pred. No. 4.4e-104;  
Matches 433; Conservative 1; Mismatches 40; Indels 1; Gaps 1;

QY 456 TGTGGGACAAAGAAATTTGAAGGAAACATGACTTTGGGAAGATCAAAATTTGAAGAGTGCAAT 515  
DB 601 TGTATGGACAAAGAAATATGAAGGAAACGAGCTTTGGGAAGATCAAAATTTGAAGAGTGCAAT 542  
QY 516 GTACATTTTCAAAATATGACTGTAAACATGAGTAGCAAACTTAGTACCCCTTCACTCTGACCCCT 575  
DB 541 GTACATTTTCAAAATATGACTGTAAACATGAGTAGCAAACTTTAGTACCCCTTCACTCTGACCCCT 482  
QY 576 ACTATCTTTTATGCTGTAAATCTGTTCTTTGTTGTAACATCTCAAGAGATGCACTCCA 635  
DB 481 GATATCTTTTCTGCTGTTAAATCTGTTCTGTTGTAACATCTCAAGAGATGCACTCCA 422  
QY 636 TGGTAAAGGATCTCAAGATCCAGACCAAGGTCACATAAAGCTTTTGGCAAACTGTGAT 695  
DB 421 TGGCAAGGATCTCAAGATCCAGACCAAGGTCACATAAAGCTTTTGGCAAACTGTGAC 362  
QY 696 CTCCTTCTCTGTTATGTCATTTACTTTCTGTCCTAATATGATATCAGTTTGGAGTTT 755  
DB 361 CTCCTTCTCTGTTATGTCATTTACTTTCTGTCCTATGATCATATCAGTTTGTAAATTT 302  
QY 756 TGGAGTCTGGAAACAAACCTGCTCTCTGTTCTGTCCTAAGCTATTAGATTCAGCTATCC 815  
DB 301 KGGGAGGCTGGAAACAAACCTGCTCTCTGTTCTGTCCTAAGCTATTATATTCAGCTATCC 242  
QY 816 TTCAATCCACCCATTCATCTCTGATTTGGGAAACAAAGAGCTTAAAGCAGACTTTTCTTTTC 875  
DB 241 TTCACCCACCCATTCATCTCTGATTTTGGGAAACAAAGAGCTTAAAGCAGACTTTTCTTTTC 182  
QY 876 AGTTTTTGGCAAAATGAGGTACTGGGTGAAAGAGAGAGACTTTCATCTCCATAG 930  
DB 181 AGTTTTTGGCGATGTGAGGTACTGGGTGAAA-GACAGAAGCCTTCGTCTCCATAG 128

RESULT 14  
US-09-949-016-108439/c  
; Sequence 108439, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 108439  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-108439

Query Match 40.8%; Score 379; DB 3; Length 601;  
Best Local Similarity 82.8%; Pred. No. 1.8e-98;  
Matches 433; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCAATTTTCCAGTCTGCTAGTGTGATCATTTTGTATTGGA 60  
DB 523 ATGATGAGTTTTTCTACACAAATGTTTTTCCATTTCTAGTAGTGTGCTATTTATTTCTTGA 464  
QY 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAG 120

DB 463 AATTTTGCATATGCTTTTATAGCACTGATATAAATTTTATTGCTGGTCAAGAGACAAAAG 404  
QY 121 ATCTCCTTTTGTGACCAAAATTTCTACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTCTGG 180  
DB 403 ATCTCCTCAGCTGATCAAAATTTATTGCTGCTCTGGCAGTCTCCAGAGTTGGTTTGTCTCTGG 344  
QY 181 GTATTATTATTAAACTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240  
DB 343 GTATATTATTATACATTGGTATTCACTGTGTGAATCCACTGCATCTAAATTTAAAGTA 284  
QY 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTCTACT 300  
DB 283 ATAAATTTTATTCTAATGCTGGGCACTAACCAATCAATTTTCAGCATCTGGCTTCTACT 224  
QY 301 ACCCTCAGCATATTTTATTGCTCAAGATGCGCAATTTCTCAACTTTTATTCTTCTTCCAC 360  
DB 223 AGCCTCAGCATATTTTATTGCTCAAGATGCGCAATTTCTCAACTTTTATTCTTCTTCCAC 164  
QY 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGCTGTGATTTGTTGGGGCTTTTGTCTATTTTGTG 420  
DB 163 TTAAGAGGAGAGTTAAGAGTGTGATTTCTGCTGTGATTTGTTGGGGCTTTTGTCTATTTTGTG 104  
QY 421 GCTTGTCTATCTTTTGTGATAAATCAATGAATGAGATTTGCGGACAAAAGAAATTTGAAGGA 480  
DB 103 GTTTGTCACTTTGTGATGAAACACACGTTATATAATGTGTGACAGAGAATGTGAAGGA 44  
QY 481 AACATGACTTGGAAATCAAAATTTGAAGTGTGCAATGTACTTTT 523  
DB 43 AACGTAATTTGGAAGATCAAACTGAGGAATGCAATGCACCTTT 1

RESULT 15  
US-09-949-016-108443/c  
; Sequence 108443, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 108443  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-108443

Query Match 39.7%; Score 368.8; DB 3; Length 601;  
Best Local Similarity 81.5%; Pred. No. 1.5e-95;  
Matches 427; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 407 CTTTGTCTATTTTGTGGCTTGTCTCATCTTTTGTGATAAACATGAATGAGATTTGCGGACAA 466  
DB 600 CTTTGTCTTTTGTGGCTTGTCTCATCTTTTGTGATAAACATGAATGAGATTTGCGGACAA 541  
QY 467 AAGAATTTGAAGGAAACATGACTTTGGAAGATCAAAATTTGAAGAGTCAATGTACTTTCAA 526  
DB 540 AAGAATTTGAAGGAAACATGACTTTGGAAGATCAAAATTTGAAGAGTCAATGTACTTTCAA 481  
QY 527 ATATGACTGTAAACCACTGTTAGTAACTTAGTAACTTCACTCTGACCCCTTACTATCTTTTA 586  
DB 480 ACTTGACTGTAGCCATGCTAGCAAACTTTGATACCAATTTACTCTGACCCCTGATATCTTTTC 421  
QY 587 TGCTGTAACTCTGTTTCTTTTGTGTAACATCTCAAGAGATGCGCTCCATGTTAAAGGAT 646

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||||| 420 TGTGTTAACTACTCTCTGTGTAAACATCTGAAGAGATGAGCTCCATGGCAAAGGAT 361
Qy ||||| 647 CTCAGATCCCGACGACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTTCCTCT 706
Db ||||| 360 CTCAGATCCCGACGACCAAGATCCACATAAAAGCTCTGCAAACTGTGACCTCCTTCCTCR 301
Qy ||||| 707 TGTATGTGCCATTACTTTCTGTCCATAAATGATATCAGTTTGGAGTTTGGAAAGTCTGG 766
Db ||||| 300 TATTACTTGGCAATTTACTTTCTGTCTTAATCATATCGTTTGGAAATTTAAGATGCTAC 241
Qy ||||| 767 AABACAAACCTGTCTTCAATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCATCCACC 826
Db ||||| 240 CAAAAGAAATGTCTTAATGCTTTGCCAAGCTTTTGGAAATCATATATCCATCTCCACT 181
Qy ||||| 827 CATTCACTCTGATTTGGGGAACAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTTCAGTTTGGC 886
Db ||||| 180 CATTCACTCTGATTTGGGGAACAAGAGCTTAAGCAGACCTTTCTTTTCAGTTTTCAGTTTGGC 121
Qy ||||| 887 AATGAGGTACTGGGTGAAGGAGAGAGACTTCATCTCCATAG 930
Db ||||| 120 AGGTGACTTGTGGGCAAAAGGACAGAACCAAGTCAACTCCATAG 77
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2006, 07:22:47 ; Search time 846 Seconds  
(without alignments)  
9090.451 Million cell updates/sec

Title: US-09-825-882-7

Perfect score: 930

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA Main.\*
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  - 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	930	100.0	930	3	US-09-825-882-7
2	930	100.0	930	6	US-10-191-058-6
3	930	100.0	930	7	US-10-343-650A-681
4	930	100.0	930	8	US-10-724-208-7
5	930	100.0	930	8	US-10-770-127-178
6	930	100.0	930	8	US-10-724-209-7
7	930	100.0	930	9	US-10-986-871-7
8	930	100.0	1330	6	US-10-017-161-1835
9	930	100.0	1330	6	US-10-292-798-1491
10	851.6	91.6	930	3	US-09-825-882-11
11	851.6	91.6	930	7	US-10-343-650A-691
12	851.6	91.6	930	8	US-10-724-208-11
13	851.6	91.6	930	8	US-10-770-127-182
14	851.6	91.6	930	8	US-10-724-209-11
15	851.6	91.6	930	9	US-10-986-871-11
16	851.6	91.6	971	5	US-10-219-834-5
17	851.6	91.6	1330	6	US-10-017-161-1837
18	851.6	91.6	1330	6	US-10-292-798-1493
19	829.2	89.2	930	3	US-09-825-882-19
20	829.2	89.2	930	8	US-10-724-208-19
21	829.2	89.2	930	8	US-10-770-127-190
22	829.2	89.2	930	8	US-10-724-209-19
23	829.2	89.2	930	9	US-10-986-871-19

24	829.2	89.2	1330	6	US-10-017-161-1931	Sequence 1931, Ap
25	829.2	89.2	1330	6	US-10-292-798-1583	Sequence 1583, Ap
26	822.8	88.5	1300	6	US-10-292-798-1479	Sequence 1479, Ap
27	819.6	88.1	1300	6	US-10-017-161-1823	Sequence 1823, Ap
28	799.6	86.0	1360	6	US-10-017-161-1825	Sequence 1825, Ap
29	799.6	86.0	1360	6	US-10-292-798-1481	Sequence 1481, Ap
30	796.4	85.6	960	6	US-10-191-058-4	Sequence 4, Appl
31	796.4	85.6	960	6	US-10-343-650A-667	Sequence 667, App
32	795	85.5	900	7	US-10-343-650A-669	Sequence 669, App
33	773.2	83.1	930	3	US-09-510-332-57	Sequence 57, Appl
34	773.2	83.1	930	8	US-10-770-127-57	Sequence 57, Appl
35	773.2	83.1	930	9	US-10-962-365-57	Sequence 57, Appl
36	751.6	80.8	960	3	US-09-510-332-52	Sequence 52, Appl
37	751.6	80.8	960	8	US-10-770-127-52	Sequence 52, Appl
38	751.6	80.8	960	9	US-10-962-365-52	Sequence 54, Appl
39	751.4	80.8	900	3	US-09-510-332-54	Sequence 54, Appl
40	751.4	80.8	900	8	US-10-770-127-54	Sequence 54, Appl
41	751.4	80.8	900	9	US-10-962-365-54	Sequence 54, Appl
42	741.2	79.7	930	3	US-09-510-332-61	Sequence 61, Appl
43	741.2	79.7	930	8	US-10-770-127-61	Sequence 61, Appl
44	741.2	79.7	930	9	US-10-962-365-61	Sequence 61, Appl
45	735.8	79.1	930	3	US-09-510-332-63	Sequence 63, Appl

## ALIGNMENTS

### RESULT 1

US-09-825-882-7  
; Sequence 7, Application US/09825882  
; Patent No. US20020094551A1  
; GENERAL INFORMATION:  
; APPLICANT: ADLER, JON ELLIOT  
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME  
; FILE REFERENCE: 078003/0279152/RXT  
; CURRENT APPLICATION NUMBER: US/09/825,882  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195,532  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/247,014  
; PRIOR FILING DATE: 2000-11-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-825-882-7

Query Match	100.0%	Score 930;	DB 3;	Length 930;
Best Local Similarity	100.0%;	Pred. No. 1.8e-245;		
Matches 930;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGATAACTTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA	60	
Db	1	ATGATAACTTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA	60	
Qy	61	AATTTTCTAATGGCTTCATAGCACTGTAAATTCATTGAGTGGTTCAAGACACAAAG	120	
Db	61	AATTTTCTAATGGCTTCATAGCACTGTAAATTCATTGAGTGGTTCAAGACACAAAG	120	
Qy	121	ATCTCTTCTGCTGACCAAAATTTCTACCTGCTCTGCGGTCTCCAGAGTTGGTTGCTCTGG	180	
Db	121	ATCTCTTCTGCTGACCAAAATTTCTACCTGCTCTGCGGTCTCCAGAGTTGGTTGCTCTGG	180	
Qy	181	GTATTATTATAACTGGTATTCACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAGTA	240	
Db	181	GTATTATTATAACTGGTATTCACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAGTA	240	
Qy	241	AGAACTACTGCTTATAATATCTGGGAGTGTATCAACCAATTTTCAGCAACTGGCTGCTACT	300	
Db	241	AGAACTACTGCTTATAATATCTGGGAGTGTATCAACCAATTTTCAGCAACTGGCTGCTACT	300	





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; Sequence 681, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 681
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-10-343-650A-681

Query Match
Best Local Similarity 100.0%; Score 930; DB 7; Length 930;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTCAGTCTGGTAGTGTACATTTGTTATTGGA 60
DB 1 ATGATAACTTTTCTACCCATCATTTTTCAGTCTGGTAGTGTACATTTGTTATTGGA 60
QY 61 AATTTTGTAAATGGCTTCATAGACATCTGGTAAATTCATTGAGTGGTTCAAGACAAAAG 120
DB 61 AATTTTGTAAATGGCTTCATAGACATCTGGTAAATTCATTGAGTGGTTCAAGACAAAAG 120
QY 121 ATCTCTTGTGTCACCAATTCCTACCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
DB 121 ATCTCTTGTGTCACCAATTCCTACCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
QY 181 GTATTATTATTAATCTGGTATTAACAATCCAGCTTTTAAATAGTGTAGAAGTA 240
DB 181 GTATTATTATTAATCTGGTATTAACAATCCAGCTTTTAAATAGTGTAGAAGTA 240
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DB 241 AGAATCTAGCTTTTATGATGCTTCACTCTGACCTTCACTCTGACCTTCACTCTGACCT 300
QY 301 ACCCTCAGCATATTTTATGCTCAAGATGGCAATTTCTCCAACTTTATTTTCTTCAC 360
DB 301 ACCCTCAGCATATTTTATGCTCAAGATGGCAATTTCTCCAACTTTATTTTCTTCAC 360
QY 361 TTTAAGAGGAGAGTTAAGAGTGTCAATTCGTGTGATGTTGGGGCCTTTGCTATTTTG 420
DB 361 TTTAAGAGGAGAGTTAAGAGTGTCAATTCGTGTGATGTTGGGGCCTTTGCTATTTTG 420

; Sequence 681, Application US/10724208
; Publication No. US20040209313A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/724,208
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-208-7

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Best Local Similarity 100.0%; Score 930; DB 8; Length 930;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTCAGTCTGGTAGTGTACATTTGTTATTGGA 60
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QY 61 AATTTTGTAAATGGCTTCATAGACATCTGGTAAATTCATTGAGTGGTTCAAGACAAAAG 120
DB 61 AATTTTGTAAATGGCTTCATAGACATCTGGTAAATTCATTGAGTGGTTCAAGACAAAAG 120
QY 121 ATCTCTTGTGTCACCAATTCCTACCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
DB 121 ATCTCTTGTGTCACCAATTCCTACCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
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DB 181 GTATTATTATTAATCTGGTATTAACAATCCAGCTTTTAAATAGTGTAGAAGTA 240
QY 241 AGAATCTAGCTTTTATGATGCTTCACTCTGACCTTCACTCTGACCTTCACTCTGACCT 300
DB 241 AGAATCTAGCTTTTATGATGCTTCACTCTGACCTTCACTCTGACCTTCACTCTGACCT 300
QY 301 ACCCTCAGCATATTTTATGCTCAAGATGGCAATTTCTCCAACTTTATTTTCTTCAC 360
DB 301 ACCCTCAGCATATTTTATGCTCAAGATGGCAATTTCTCCAACTTTATTTTCTTCAC 360
QY 361 TTTAAGAGGAGAGTTAAGAGTGTCAATTCGTGTGATGTTGGGGCCTTTGCTATTTTG 420
DB 361 TTTAAGAGGAGAGTTAAGAGTGTCAATTCGTGTGATGTTGGGGCCTTTGCTATTTTG 420

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; SEQ ID NO 1491
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1330)
; NAME/KEY: CDS
; LOCATION: (201)..(1130)
US-10-292-798-1491

Query Match      100.0%; Score 930; DB 6; Length 1330;
Best Local Similarity 100.0%; Pred. No. 2.2e-245;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db 201 ATGATAACTTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 260
QY 61 AATTTTGCTAATGGCTTCATAGCACTGTAATCCATTGAGTGGTTCAAGAGACAAAG 120
Db 261 AATTTTGCTAATGGCTTCATAGCACTGTAATCCATTGAGTGGTTCAAGAGACAAAG 320
QY 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 321 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 380
QY 181 GTATTATTATAAAGTGTATTAATCTGATGTTGAATCCAGCTTTTAATAGTGTAGAAGTA 240
Db 381 GTATTATTATAAAGTGTATTAATCTGATGTTGAATCCAGCTTTTAATAGTGTAGAAGTA 440
QY 241 AGAACTACTGCTTATAATATCTGGGCGAGTGATCAACCAATTTTCAGCACTGGCTTGCTACT 300
Db 441 AGAACTACTGCTTATAATATCTGGGCGAGTGATCAACCAATTTTCAGCACTGGCTTGCTACT 500
QY 301 ACCCTCAGCAATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTTATTTTCTTCAAC 360
Db 501 ACCCTCAGCAATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTTATTTTCTTCAAC 560
QY 361 TTAAGAGGAGAGTAAAGAGTGTCAATCTGATGTTGTTGGGCGCTTGCTATTATTG 420
Db 561 TTAAGAGGAGAGTAAAGAGTGTCAATCTGATGTTGTTGGGCGCTTGCTATTATTG 620
QY 421 GCTTGTCACTTTTGTGATAAACAATGAATGAGATTGTCGCGACAAAGAATTTGAAGGA 480
Db 621 GCTTGTCACTTTTGTGATAAACAATGAATGAGATTGTCGCGACAAAGAATTTGAAGGA 680
QY 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGCATTTCTTTTCAAAATATGACTGTAACC 540
Db 681 AACATGACTTTGGAAGATCAAAATGAAGAGTGCATTTCTTTTCAAAATATGACTGTAACC 740
QY 541 ATGGTAGCAAACTTAGTACCCCTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
Db 741 ATGGTAGCAAACTTAGTACCCCTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 800
QY 601 TCTTTGTGTAACAATCTCAAGAGATGCAGCTCCATGTAAGGATCTCAAGATCCCGAGC 660
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QY 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTTATCCCTTCAATCCACCCATTCATCTGATT 840
Db 981 TTCAATGTTCTGCAAGCTATTAGATTCAGCTTATCCCTTCAATCCACCCATTCATCTGATT 1040
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QY 841 TGGGAAACAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTTTTGGCAATGAGGTACTGG 900
Db 1041 TGGGAAACAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTTTTGGCAATGAGGTACTGG 1100
QY 901 GTGAAGGAGAGAGAGACTTCATCTCCATAG 930
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RESULT 10
US-09-825-882-11
; Sequence 11, Application US/09825882
; Patent No. US20020094551A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/EXT
; CURRENT APPLICATION NUMBER: US/09/825,882
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-882-11

Query Match      91.6%; Score 851.6; DB 3; Length 930;
Best Local Similarity 94.7%; Pred. No. 7.4e-224;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db 1 ATGCAACTTTTATATACCCATCAATTTTCCAGTCTGGTAGTGGTTCTATTCTGTTATTGGA 60
QY 61 AATTTTGCTAATGGCTTCATAGCACTGTAATCCATTGAGTGGTTCAAGAGACAAAG 120
Db 61 AATTTTGCTAATGGCTTCATAGCACTGTAATCCATTGAGTGGTTCAAGAGACAAAG 120
QY 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
QY 181 GTATTATTATAAAGTGTATTAATCTGATGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 181 GTATTATTATAAAGTGTATTAATCTGATGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
QY 241 AGAACTACTGCTTATAATATCTGGGCGAGTGATCAACCAATTTTCAGCACTGGCTTGCTACT 300
Db 241 AGAACTACTGCTTATAATATCTGGGCGAGTGATCAACCAATTTTCAGCACTGGCTTGCTACT 300
QY 301 ACCCTCAGCAATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTTATTTTCTTCAAC 360
Db 301 AGCTCTCAGCAATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTTATTTTCTTCAAC 360
QY 361 TTAAGAGGAGAGTAAAGAGTGTCAATCTGATGTTGTTGGGCGCTTTGCTATTATTTTG 420
Db 361 TTAAGAGGAGAGTAAAGAGTGTCAATCTGATGTTGTTGGGCGCTTTTACTATTATTTTG 420
QY 421 GCTTGTCACTTTTGTGATAAACAATGAATGAGATTGTCGCGACAAAGAATTTGAAGGA 480
Db 421 GCTTGTCACTTTTGTGATAAACAATGAATGAGATTGTCGCGACAAAGAATTTGAAGGA 480
QY 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGCATTTCTTTTCAAAATATGACTGTAACC 540
Db 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGCATTTCTTTTCAAAATATGACTGTAACC 540
QY 541 ATGGTAGCAAACTTAGTACCCCTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
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Db 541 ACCTAGGAACTTAGTGCCCTTCACTCTGACCCCTGCTATGTTTTTGTGCTTAATCTGT 600  
Qy 601 TCTTTGTGTAACATCTCAAGAAGATGAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660  
Db 601 TCTCTGTGTAACATCTCAAGAAGATGAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660  
Qy 661 ACCAAGGTCACATAAAGCTTTGCAACCTGTGATCTCTCTCTTTGTTATGTGCCATT 720  
Db 661 ACCAAGGTCACATAAAGCTTTGCAACCTGTGATCTCTCTCTTTGTTATGTGCCATT 720  
Qy 721 TACTTTCTGTCATATATGATATCAGTTTGGAGTTTGGAGTCTGGAAAAAACAACCTGTC 780  
Db 721 TACTTTCTGTCATATATGATATCAGTTTGGAGTTTGGAGTCTGGAAAAAACAACCTGTC 780  
Qy 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTTCATCTGATT 840  
Db 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTTCATCTGATT 840  
Qy 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTTTTTGGCAATGAGTACTGG 900  
Db 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTTTTTGGCAATGAGTACTGG 900  
Qy 901 GTGAAGGAGAGAAGACTTTCATCTCCATAG 930  
Db 901 GTGAAGGAGAGAAGCTTTCATCTCCATAG 930

RESULT 11  
US-10-343-650A-691  
; Sequence 691, Application US/10343650A  
; Publication No. US20040067499A1  
; GENERAL INFORMATION:  
; APPLICANT: HAGA, TATSUYA  
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: 31671-186347  
; CURRENT APPLICATION NUMBER: US/10/343,650A  
; PRIOR FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: JP 2000/237818  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: JP 2001/34434  
; PRIOR FILING DATE: 2001-02-13  
; NUMBER OF SEQ ID NOS: 694  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 691  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(930)  
US-10-343-650A-691

Query Match 91.6%; Score 851.6; DB 7; Length 930;  
Best Local Similarity 94.7%; Pred. No. 7.4e-224;  
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
Qy 1 ATGTAACCTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTCTGTTATGGA 60  
Db 1 ATGACAACCTTTTATACCCCATCATTTTTTCCAGTGTGGTAGTGGTTCTATTGTTATGGA 60  
Qy 61 AATTTTGTCTAATAGGCTTCATAGCACCTGGTAAATTCATTGAGTGGTTCAAGACAAAAAG 120  
Db 61 AATTTTGTCTAATAGGCTTCATAGCATTTGGTAATTCATTGAGCGGTCAAGACAAAAAG 120  
Qy 121 ATCTCTTTTGTGACCAAAATTCCTACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180  
Db 121 ATCTCTTTTGTGACCAAAATTCCTACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180  
Qy 181 GTATTATTATTAACTGGTATTCAACTGTTGTAATCCAGCTTTTAATAGTAGTAGAAGTA 240  
Db 181 GTATTATTATTAACTGGTATTCAACTGTTGTAATCCAGCTTTTATATAGTAGTAGAAGTA 240  
Qy 241 AGAACTACTGCTTATAATATCTGGGCAGTGATCAACCACTTTCAGCAACTGGCTTGCTACT 300

Db 241 AGAACTACTGCTTATAATGCTTGGGCACTAACCGCCATTTTCAGCAACTGGCTTGCTACT 300  
Qy 301 ACCCTCAGATATTTTATTTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCCAC 360  
Db 301 AGCTTCAGATATTTTATTTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCCAC 360  
Qy 361 TTAAGAGGAGATTAAGAGTCTCAATCTGTTGATGTTGTTGGGCGCTTTGCTATTTTGG 420  
Db 361 TTAAGAGGAGATTAAGAGTCTCAATCTGTTGATGTTGTTGGGCGCTTTTACTATTTTGG 420  
Qy 421 GCTTGTCTATCTTTTGTGATAAAACATGAATGAGATTTGTGCGACAAAAAGAAATTGAAGA 480  
Db 421 GCTTGTCTCAACTTTTGTGATAAAACATGAAGAGATTGTACGCGACAAAAAGAAATGAAGA 480  
Qy 481 AACATGACTTGAAGATCAAAATTGAAGAGTGCATGTACTTTTCAAAATATGATCTGAACC 540  
Db 481 AACTTGACTTGAAGATCAAAATTGAAGAGTGCAGTGTACCTTTTCAGATGCGACTGTAAACC 540  
Qy 541 ATGTTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600  
Db 541 AGCTTAGGAACCTTAGTGCCTTCACTCTGACCCCTGCTATGTTTTTGTGCTGTTAATCTGT 600  
Qy 601 TCTTTGTGTAAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660  
Db 601 TCTCTGTGTAAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660  
Qy 661 ACCAAGTCCACATAAAAAGCTTTGCAAACTGTGATCTCTCTCTTGTATTGTGCCATT 720  
Db 661 ACCAAGTCCACATAAAAAGCTTTGCAAACTGTGATCTTTTCTCTTGTATTGTGCCATT 720  
Qy 721 TACTTTCTGCCATAATGATATCAGTTTGGAGTCTTGGAAAGTCTGGAAAAAACAACCTGTC 780  
Db 721 TACTTTCTGCCATAATGATATCAGTTTGGAGTCTTGGAGTCTGGAAAAAACAACCTGTC 780  
Qy 781 TTTCACTTCTTGCAAAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTTCATCTGATT 840  
Db 781 TTTCACTTCTTGCAAAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTTCATCTGATT 840  
Qy 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTTTTTGGCAATGAGTACTGG 900  
Db 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTTTTTGGCAATGAGTACTGG 900  
Qy 901 GTGAAGGAGAGAAGACTTTCATCTCCATAG 930  
Db 901 GTGAAGGAGAGAAGCTTTCATCTCCATAG 930

RESULT 12  
US-10-724-208-11  
; Sequence 11, Application US/10724208  
; Publication No. US20040209313A1  
; GENERAL INFORMATION:  
; APPLICANT: ADLER, JON ELLIOT  
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME  
; FILE REFERENCE: 078003/0279152/RXT  
; CURRENT APPLICATION NUMBER: US/10/724,208  
; CURRENT FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: 60/195,532  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/247,014  
; PRIOR FILING DATE: 2000-11-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-724-208-11

Query Match 91.6%; Score 851.6; DB 8; Length 930;  
Best Local Similarity 94.7%; Pred. No. 7.4e-224;  
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;









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Qy 181 GTATTATTATTAAACTGGTATTCAACTGTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 181 GTATTATTATTAAATTTGGTATTCAACTGTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Qy 241 AGAACTACTGCTTATAATATCTGGGAGTGTATCAACCAATTTTCAGCACTGGCTGCTACT 300
Db 241 AGAACTACTGCTTATAATATCTGGGAGTGTATCAACCAATTTTCAGCACTGGCTGCTACT 300
Qy 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCAC 360
Db 301 AGCCTCAGCATATTTTATTGCTCAGATTCGCAATTTCTCCAACTTTATTTTCTTCAC 360
Qy 361 TTAAGAGGAGAGTTAAGAGTGTATCTGTGTATGTTGGGGCCCTTTGCTATTTTGG 420
Db 361 TTAAGAGGAGAGTTAAGAGTGTATCTGTGTATGTTGGGGCCCTTTGCTATTTTGG 420
Qy 421 GCTTGTCTATCTTTTGTGATAAACATGAATGAGATGTACTTTTCAAAATATGACTGTAAAC 480
Db 421 GCTTGTCAACTTTTGTGATAAACATGAAGAGATGTACTTTTCAAAATATGACTGTAAAC 480
Qy 481 AACATGACTTTGGAAGATCAAAATGGAAGTGTCAATGTACTTTTCAAAATATGACTGTAAAC 540
Db 481 AACTTGTACTTGAAGATCAAAATGGAAGTGTCAATGTACTTTTCAAAATATGACTGTAAAC 540
Qy 541 ATGCTAGCAACTTTAGTACCCCTTCACTGTGACCCCTTCACTGTGACCCCTTCACTGTGACCCCTT 600
Db 541 ACCTAGCAACTTTAGTACCCCTTCACTGTGACCCCTTCACTGTGACCCCTTCACTGTGACCCCTT 600
Qy 601 TCTTTGTGTAACATCTCAAGAGATGAGTGTCAATGAGTGTCAATGAGTGTCAATGAGTGTCAAT 660
Db 601 TCTCTGTGTAACATCTCAAGAGATGAGTGTCAATGAGTGTCAATGAGTGTCAATGAGTGTCAAT 660
Qy 661 ACCAAGTCCACATATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 661 ACCAAGTCCACATATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Qy 721 TACTTTCTGTCATATAATGATATCAAGTGTGGAGTTTGGAGTGTGGAGTGTGGAGTGTGGAGTGT 780
Db 721 TACTTTCTGTCATATAATGATATCAAGTGTGGAGTTTGGAGTGTGGAGTGTGGAGTGTGGAGTGT 780
Qy 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCATCCTGATT 840
Db 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCATCCTGATT 840
Qy 841 TGGGAAACAAGAGCTAAAGCAGACTTTTCTTTGAGTTTGGCAAAATGAGGTACTGG 900
Db 841 TGGGAAACAAGAGCTAAAGCAGACTTTTCTTTGAGTTTGGCAAAATGAGGTACTGG 900
Qy 901 GTGAAGGAGAGAGACTTTCATCTCCATAG 930
Db 901 GTGAAGGAGAGAGCCCTTCATCTCCATAG 930

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Search completed: May 1, 2006, 08:57:51  
Job time : 848 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
C	1	457.8	49.2	599	7	US-09-325-065A-489444
	2	419.4	45.1	622	12	US-10-301-480-376959
	3	419.4	45.1	622	12	US-10-301-480-990368
	4	418.2	45.0	632	12	US-10-301-480-376958
	5	418.2	45.0	632	12	US-10-301-480-990367
	6	417.8	44.9	632	12	US-10-301-480-376957
	7	417.8	44.9	632	12	US-10-301-480-990366
	8	416.4	44.8	619	7	US-09-325-065A-300419
	9	415.2	44.6	619	7	US-09-325-065A-300418
	10	414.8	44.6	619	7	US-09-325-065A-300417
C	11	411	44.2	525	12	US-10-301-480-250660
	12	411	44.2	525	12	US-10-301-480-864069
	13	398.6	42.9	612	12	US-10-301-480-251369
	14	398.6	42.9	612	12	US-10-301-480-864778

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Qy	191	TAAACTGCTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAAGTAAGAACTACTG	250
Db	539	TCCTTTGGTATGCAACTGTGTGTTAAATTCGCTTTATATGCTTTAGAAAGTAAGAAATGTTG	480
Qy	251	CTTTAATAATCTGGGCGAGTGATCAACCATTTTACGCAACTGGCTTGCTACTACCCCTCAGCA	310
Db	479	CTTCTTAATGCGCTGGGCTGTAAAGCAACCATTTTACGCAATGTGGCTTGCTGTAGCCTCAGCA	420
Qy	311	TATTTTATTTTGTCTCAAGATTGCGCAATTTCTCCAACTTTATTTTCTTCTCACTTAAAGAGGA	370
Db	419	TATTTTGTGTTGCTCAAGATTGCGCAATTTCTCCAACTTATTTCTCCACCTTAAGAGGA	360
Qy	371	GAGTTAAGAGTGTCAATCTGGTGATGTGTGGGGCCTTTGGCTATTATTTTGGCTTGTCAATC	430
Db	359	GAAATTAAGAGTGTGTGTTCTGGTGATCTGTGGGGCCCTTGGTATTATTTTGATTTGTAAATC	300
Qy	431	TTTTTGTGATAAACAATGAATGAGATTGTGCGGCAAAAGAAATTTGAAGGAAACATGACTT	490
Db	299	TTGCTGTGATAACCAATGGATGAGAGAGTGTGGAACAAAGAAATATGAAGGAAATGTGACTT	240
Qy	491	GGAAGATCAAAATTTGAAGAGTGCAAATGTACTTTTCAAAATAGACTGTAAACCATGGTAGCA	550
Db	239	GGAAGATCAAAATTTGAGGAATGCAATACACTTTCAAGCTTGACTGTAACTACTCTAGCAA	180
Qy	551	ACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTATGCTGTTAAATCTGTTCTTTTGTA	610
Db	179	ACCTCATACCCCTTACTCTGAGCGCTAATATGTTTCTGCTGTTAAATCTGTTCTCTTTGTA	120
Qy	611	AACATCTCAAGAAGATGCAAGCTCCATGGTTAAAGGATCTCAAGATCCCAAGCAACCAAGTCC	670
Db	119	AACATCTCAAGAAGATGCGGCTCCATAGCAAAAGGATCTCAAGATCCCAAGCAACCAAGTCC	60
Qy	671	ACATAAAAGCTTTGCAAACTGTGATCTCCCTTCTCTGTTATGTGGCATTTACTTTCTG	729
Db	59	ATATAAAAGCTTTGCAAACTGTGACTCTCTCTCATGTTATTTGGCAATTTACTTTCTG	1

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RESULT 2
US-10-301-480-376959
; Sequence 376959, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376959
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-376959

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RESULT 3
US-10-301-480-990368
; Sequence 990368, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIORITY APPLICATION NUMBER: US 10/215,598
; PRIORITY FILING DATE: 2002-08-09
; PRIORITY APPLICATION NUMBER: US 60/311,695
; PRIORITY FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 990368
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-990368

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121	DB	CAAAATTTCTCAGTCTCTGCTGGTGTCCAGAGTTGGTTTAACTCTCGGGTCATATTATTACA	180
195	QY	CTGGTATTTCAACTGCTGTTTGAATCCAGCTTTTAAATAGTCTAGAAGTAAGAACTACTGCTTA	254
181	DB	TTGGTATGCAACTGCTGTTTAAATTTGGCTTCACATAGATTAGAAGTAAAGATTTTGGTTC	240
255	QY	TAATATCTGGGCAGTGATCAACCAATTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT	314
241	DB	TAATGTCTCAGCAATAACCAAGCATTTTCAGCATCTGG-GTGTTACTAGGCTCAGCATATT	299
315	QY	TTATTTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTTCTTCACTTAAAGAGGAGT	374
300	DB	TCAATTTGCTCAAGATTCGCAATTTCTCCAGCTTATTTTTCTCCACCTAAAGAARAGGAT	359
375	QY	TAAAGATGTCAATCTCGTGTGATGTTGTGGGGCCCTTTGCTATTTTGGCTTGTCATCTTTT	434
360	DB	TAGAAATGTGGTTTGGTGATGCTGTGTGGGGCCCTTGGTATTTTTCATTTGTAAATCTTGC	419
435	QY	TGTGATAAACACATGAATGAGATTGTGCGGACAAAAGAAATTTGAAGAAACATGACTTTGGAA	494
420	DB	TCTGATAAACACGGGTGAGAGTGTGTGGACAAAAGAAATATGAAGGAAATTTGCTTTGGAT	479
495	QY	GATCAAAATTTGNAGAGTGCATGTACTTTTTCAAAATAGACTGTAAACCATGGTAGCAAACTT	554
480	DB	GATCAAAATTTGAGGAATGCATACAGCTTTTCAAACTTGACTGTAAACATGCCAGCAAACTG	539
555	QY	AGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAACTGCTTTCTGTGTAAACA	614
540	DB	CACACCCCTGCATCTGACATTAATCTTTTCTGCTGTTAATCTAATTTCTCCATGTAAACA	599
615	QY	TCTCAAGAAGATGCAGTCCATG	637
600	DB	TGTCAAGAAGATGCAGTCCATG	622

	Query Match	45.1%	Score 419.4;	DB 12;	Length 622;
	Best Local Similarity	81.5%	Pred. No. 2.3e-89;		
	Matches 508;	Conservative 1;	Mismatches 112;	Indels 2;	Gaps 2
Qy	16	CCCATCATTTTTTCCAGTCTCGTAGTGGTTACATTTGTTATTGGAAATTTTGTCTAATGGC	75		
Db	1	CTCATCATTTTATCAATCTCGTAGTGGTTGCAATTTCTTTGGAAATGTTGCCAATGGC	60		
Qy	76	TTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAGATCTCTTTTGTCTGAC	135		
Db	61	TTCATAGCTCTAGTAGGTGTCCTTGAGTGGGTTAAGACACAAAGATCTCATCAGCTGAC	120		
Qy	136	CAAA-TTCTCACTGCTCGGCGGTCTCCAGAGTTGGTTTGCTCTGGGTATTATTATAA	194		

Db 121 CAAATTTCTCACTGCTCTGGTGTCCAGAGTTGGTTTACTCTGGGTCAATATTATACA 180  
QY 195 CTGTAATCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254  
Db 181 TTGGTATGCAACTGTGTTTAAATTTGGCTTCACATAGATTAGAAATTTTGGTTC 240  
QY 255 TAATATCTGGGCACTGATCAACCAATTTTCCAGAACTGGCTTGTCTACTACCTCAGCATATT 314  
Db 241 TAATGTCTCAGCAATAACCAAGCAATTTTCCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299  
QY 315 TTATTTGCTCAAGATTCGCAATTTCTCAACTTTTAAATTTTCTTCACTTTAAAGAGGAGT 374  
Db 300 TCATTTGCTCAAGACTGCAATTTCTCAACTTTTAAATTTTCTTCACTTTAAAGAGGAGT 359  
QY 375 TAAGAGTGTCAATCTGGTGATGTTGTTGGGGCCCTTTTGTCTATTATTTTGGCTTGTCACTTTT 434  
Db 360 TAAGAAATGTTGGTTTGGTGATGCTGTTGGGGCCCTTGGTATTATTTTCAATTTGTAATCTTGC 419  
QY 435 TGTGATAAACAATGAATGAGATTTGGCGGACAAAAGAAATTTGAAGAAACATGACTTGGAA 494  
Db 420 TCTGATAACCAACCGGTGAGAGTGTGGACAAAAGAAATATGAAGAAATTTTGTCTTGGAT 479  
QY 495 GATCAAAATTCGAAGAGTGCATGTAATTTTCAAAATATGACTGTAAACCATGGTAGCAACTT 554  
Db 480 GATCAAAATTCGAAGATGCAATACAGCTTTCAAACTTGTAACCATGCCAGCAAACT 539  
QY 555 AGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGTTCTTTTGTGTAACA 614  
Db 540 CACACCTGCACTCTGACACTAATATCTTTTCTGCTGTAAATCTATTCTCCATGTAAACA 599  
QY 615 TCTCAAGAAGATGAGCTCCATG 637  
Db 600 TGTCAAGAAGATGAGCTCCATG 622

## RESULT 4

US-10-301-480-376958  
; Sequence 376958, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; TITLE OF INVENTION: in the Human Genome  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 376958  
; LENGTH: 622  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-376958

Query Match 45.0%; Score 418.2; DB 12; Length 622;  
Best Local Similarity 81.5%; Pred. No. 4.4e-89;  
Matches 508; Conservative 0; Mismatches 113; Indels 2; Gaps 2;

QY 16 CCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTCTTATTTGGAATTTTGTCTAATGGC 75  
Db 1 CTCATCATTTTATCAATTCCTGGTAGTGTGTCATTTGTTCTTGGAAATGTTGCCAATGGC 60  
QY 76 TTCAATAGCACTGGTAAATTCATTTAGTGGTTCAAGAGACAAAGATCTCTTTTGTCTGAC 135  
Db 61 TTCAATAGCTCTAGTAGTGTCTTGGTGGGTTAAGACACAAAGATCTCATCAGCTGAC 120  
QY 136 CAAA-TTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTCTGGGTATTATTATAA 194  
Db 121 CAAATTTCTCACTGCTCTGGTGTGTCAGAGTTGGTTTACTCTGGGTCAATATTATACA 180

QY 195 CTGTAATCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254  
Db 181 TTGGTATGCAACTGTGTTTAAATTTGGCTTCACATAGATTAGAAATTTTGGTTC 240  
QY 255 TAATATCTGGGCACTGATCAACCAATTTTCCAGAACTGGCTTGTCTACTACCTCAGCATATT 314  
Db 241 TAATGTCTCAGCAATAACCAAGCAATTTTCCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299  
QY 315 TTATTTGCTCAAGATTCGCAATTTCTCAACTTTTAAATTTTCTTCACTTTAAAGAGGAGT 374  
Db 300 TCATTTGCTCAAGACTGCAATTTCTCAACTTTTAAATTTTCTTCACTTTAAAGAGGAGT 359  
QY 375 TAAGAGTGTCAATCTGGTGATGTTGTTGGGGCCCTTTTGTCTATTATTTTGGCTTGTCACTTTT 434  
Db 360 TAAGAAATGTTGGTTTGGTGATGCTGTTGGGGCCCTTGGTATTATTTTCAATTTGTAATCTTGC 419  
QY 435 TGTGATAAACAATGAATGAGATTTGGCGGACAAAAGAAATTTGAAGAAACATGACTTGGAA 494  
Db 420 TCTGATAACCAACCGGTGAGAGTGTGGACAAAAGAAATATGAAGAAATTTTGTCTTGGAT 479  
QY 495 GATCAAAATTCGAAGAGTGCATGTAATTTTCAAAATATGACTGTAAACCATGGTAGCAACTT 554  
Db 480 GATCAAAATTCGAAGATGCAATACAGCTTTCAAACTTGTAACCATGCCAGCAAACT 539  
QY 555 AGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGTTCTTTTGTGTAACA 614  
Db 540 CACACCTGCACTCTGACACTAATATCTTTTCTGCTGTAAATCTATTCTCCATGTAAACA 599  
QY 615 TCTCAAGAAGATGAGCTCCATG 637  
Db 600 TGTCAAGAAGATGAGCTCCATG 622

## RESULT 5

US-10-301-480-990367  
; Sequence 990367, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; TITLE OF INVENTION: in the Human Genome  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 990367  
; LENGTH: 622  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-990367

Query Match 45.0%; Score 418.2; DB 12; Length 622;  
Best Local Similarity 81.5%; Pred. No. 4.4e-89;  
Matches 508; Conservative 0; Mismatches 113; Indels 2; Gaps 2;

QY 16 CCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTCTTATTTGGAATTTTGTCTAATGGC 75  
Db 1 CTCATCATTTTATCAATTCCTGGTAGTGTGTCATTTGTTCTTGGAAATGTTGCCAATGGC 60  
QY 76 TTCAATAGCACTGGTAAATTCATTTAGTGGTTCAAGAGACAAAGATCTCTTTTGTCTGAC 135  
Db 61 TTCAATAGCTCTAGTAGTGTCTTGGTGGGTTAAGACACAAAGATCTCATCAGCTGAC 120  
QY 136 CAAA-TTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTCTGGGTATTATTATAA 194  
Db 121 CAAATTTCTCACTGCTCTGGTGTGTCAGAGTTGGTTTACTCTGGGTCAATATTATACA 180

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QY 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TTGGTATGCAACTGTGTTTAAATTTGGCTTTCACATAGATTAGAGTTAGAAATTTTGGTTC 240
QY 255 TAATATCTGGGCAGTGATCAACCAATTTTCAGCAACTGGCTTGTCTACTACCCCTCAGCATATT 314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TAAATGCTCTCAGCAATAACCAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 TTATTTGCTCAAGATGCGCAATTTTCTCAACTTTATTTTCTTCACTTTAAAGAGAGAGT 374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 TCATTTGCTCAAGACTGCGCAATTTTCTCAACCTTATTTTCTCCACCTAAAGAAAAGGAT 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 TAAGAGTGTCAATCTGTGTGATGCTGTGGGGCTTTTGTCTATTTTGGCTTGTCTCTTTT 434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
360 TAAGAAATGTTGGTGTGATGCTGTGGGGCTTTTGTCTATTTTTCATTTTGAATCTTTCG 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 TGTGATAAATCATGAATGAGATTTGTGGGACAAAAGAAATTTGAAGGAAACATGACTTTGGAA 494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
420 TCTGATAACCAAGGCTGAGAGTGTGGGACAAAAGAAATATGAAGGAAATTTGTCTTGGAT 479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 GATCAAAATGAAGATGCAATGTAATTTTCAAAATGACTGTAAACCATGGTAGCAAACTT 554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 GATCAAAATGAGAAATGCAATACAGCTTTTCAAACTTTGACTGTAAACCATGCCAGCAAGCT 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 AGTACCCCTTCACTCTGACCTACTATCTTTTATGCTGTAAATCTCTTTTGTGTAAACA 614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
540 CACACCCCTGCACTCTGACACTAATATCTTTCTGCTGTTAATCTATTTCTCCATGTAAACA 599
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 TCTCAAGAAGATGCACTCCATG 637
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 TGTCAAGAAGATGCACTCCATG 622
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## RESULT 6

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US-10-301-480-376957
; Sequence 376957, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376957
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-376957
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Query Match 44.9%; Score 417.8; DB 12; Length 622;
Best Local Similarity 81.4%; Pred. No. 5.5e-89;
Matches 507; Conservative 1; Mismatches 113; Indels 2; Gaps 2;
```

```
QY 16 CCCATCATTTTTCAGTCTGGTAGTGGTTACATTTGTTATTTGGAAATTTTGTCTAATGGC 75
Db 1 CTCATCATTTTATCAATTCCTGGTAGTGGTTTGCATTTGTTTCTTGGAAATGTTGCCAATGGC 60
QY 76 TTCTAGACACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAAGATCTCTTCTGCTGAC 135
Db 61 TTCTAGACCTTAGTAGGTCTCTGAGTGGGTTAAGACACAAAAGATCTCTCATCAGCTGAC 120
QY 136 CAAA-TTCTCACTGCTGGGGCTCCAGAGTGGTTTGTCTGGGTATTTATTATAA 194
Db 121 CAAATTTCTCACTGCTGGGTGTCAGAGTGGTTTGTCTGGGTCAATATTATACA 180
QY 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254
```

```
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TTGGTATGCAACTGTGTTTAAATTTGGCTTTCACATAGATTAGAGTTAGAAATTTTGGTTC 240
QY 255 TAATATCTGGGCAGTGATCAACCAATTTTCAGCAACTGGCTTGTCTACTACCCCTCAGCATATT 314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TAAATGCTCTCAGCAATAACCAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 TTATTTGCTCAAGATGCGCAATTTTCTCAACTTTATTTTCTTCACTTTAAAGAGAGAGT 374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 TCATTTGCTCAAGACTGCGCAATTTTCTCAACCTTATTTTCTCCACCTAAAGAAAAGGAT 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 TAAGAGTGTCAATCTGTGTGATGCTGTGGGGCTTTTGTCTATTTTGGCTTGTCTCTTTT 434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
360 TAAGAAATGTTGGTGTGATGCTGTGGGGCTTTTGTCTATTTTTCATTTTGAATCTTTCG 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 TGTGATAAATCATGAATGAGATTTGTGGGACAAAAGAAATTTGAAGGAAACATGACTTTGGAA 494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
420 TCTGATAACCAAGGCTGAGAGTGTGGGACAAAAGAAATATGAAGGAAATTTGTCTTGGAT 479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 GATCAAAATGAAGATGCAATGTAATTTTCAAAATGACTGTAAACCATGGTAGCAAACTT 554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 GATCAAAATGAGAAATGCAATACAGCTTTTCAAACTTTGACTGTAAACCATGCCAGCAAGCT 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 AGTACCCCTTCACTCTGACCTACTATCTTTTATGCTGTAAATCTCTTTTGTGTAAACA 614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
540 CACACCCCTGCACTCTGACACTAATATCTTTCTGCTGTTAATCTATTTCTCCATGTAAACA 599
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 TCTCAAGAAGATGCACTCCATG 637
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 TGTCAAGAAGATGCACTCCATG 622
```

## RESULT 7

```
US-10-301-480-990366
; Sequence 990366, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 990366
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-990366
```

```
Query Match 44.9%; Score 417.8; DB 12; Length 622;
Best Local Similarity 81.4%; Pred. No. 5.5e-89;
Matches 507; Conservative 1; Mismatches 113; Indels 2; Gaps 2;
```

```
QY 16 CCCATCATTTTTCAGTCTGGTAGTGGTTACATTTGTTATTTGGAAATTTTGTCTAATGGC 75
Db 1 CTCATCATTTTATCAATTCCTGGTAGTGGTTTGCATTTGTTTCTTGGAAATGTTGCCAATGGC 60
QY 76 TTCTAGACACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAAGATCTCTTCTGCTGAC 135
Db 61 TTCTAGACCTTAGTAGGTCTCTGAGTGGGTTAAGACACAAAAGATCTCTCATCAGCTGAC 120
QY 136 CAAA-TTCTCACTGCTGGGGCTCCAGAGTGGTTTGTCTGGGTATTTATTATAA 194
Db 121 CAAATTTCTCACTGCTGGGTGTCAGAGTGGTTTGTCTGGGTCAATATTATACA 180
QY 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254
```

Db 181 TTGGTATGCAACTGTGTTTAAATTTGGCTTCACATAGATTAGAAAGTAAAGAAATTTTGGTTC 240  
Qy 255 TAATATCTGGGAGTGATCAACCAATTTTCAGCAACTGGCTTGCTACTACCTCAGCATATT 314  
Db 241 TAATGTCTCAGCAATACCAAGCAATTTTCAGCATCTGG-GTGTTACTAGCCTCAGCATATT 299  
Qy 315 TTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTTATTTTCTTCCACTTAAAGAGGAGT 374  
Db 300 TCAATTTGCTCAGACTGCCAAATTTCTCCAACTTTTATTTTCTCCACTTAAAGAAAGGAT 359  
Qy 375 TAAGAGTGTCAATTCGTGTGATGTTGGTGGGCCCTTTGCTATTTTGGCTTTGTCATCTTTT 434  
Db 360 TAAGAATGTTGGTTTGGTGATGCTGTTGGGGCCCTTGCTATTTTTCATTTGTAATCTTGC 419  
Qy 435 TGTGATAAACAATGAGATGTTGGCGGACAAAAGAAATTTGAAGGAAACATGACTTGGAA 494  
Db 420 TCTGATAACCAACGGGTGAGAGTGTGGACAAAAGAAATATCAAGGAAATTTGTCTTGGAT 479  
Qy 495 GATCAAAATTCAGAGTGCATGTACTTTTCAAAATATGACTGTAAACCATGTTAGCAAACTT 554  
Db 480 GATCAAAATTCAGGAATGCATACAGCTTTCAAACTTGACTGTAAACCATGCCAGCAACGT 539  
Qy 555 AGTACCCCTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGTTTCTTTGTGTAACA 614  
Db 540 CACACCCCTGCACCTGACACTAATATCTTTTCTGCTGTTTATCTTCTCATGTAAACA 599  
Qy 615 TCTCAAGAAGATGAGCTCCATG 637  
Db 600 TGTCAAGAAGATGAGCTCCATG 622

## RESULT 8

US-09-925-065A-300419  
; Sequence 300419, Application US/09925065A  
; Publication No. US20040181048A1

## GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 300419

; LENGTH: 619

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-300419

Query Match 44.8%; Score 416.4; DB 7; Length 619;

Best Local Similarity 81.5%; Pred. No. 1.2e-88;

Matches 505; Conservative 1; Mismatches 112; Indels 2; Gaps 2;

16 CCCATCATTTTTTCCAGTCTGGTAGTGTATACATTTGTTATGGAATTTTGTCTAATGGC 75

1 CTCATCATTTTATCAATTCGTGTAGTGTGTTGCAATTTGTTCTTGGAAATGTTGCCAATGGC 60

76 TTCATAGACCTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAAGATCTCTTGTCTGAC 135

61 TTCAATAGCTCTAGTAGGTGCTCTTGGAGTGGGTGAAGACACAAAAGATCTCATCAGCTGAC 120

136 CAAA-TTCTCACTGCTCTGGGGCTCTCAGAGTTGGTTTGTCTCTGGGTATTATTATTA 194

Db 121 CAAATTTCTCACTGCTCTGGTGGTGTCCAGAGTTGGTTTACTCTGGGTCAATATTATACA 180  
Qy 195 CTGGTATTCAACTGTGTGTAATCCAGCTTTTAAATAGTGTAGAAGTAAAGACTACTGCTTA 254  
Db 181 TTGGTATGCAACTGTGTTTAAATTTGGCTTCACATAGATTAGAAAGTAAAGAAATTTTGGTTC 240  
Qy 255 TAATATCTGGGAGTGTATCAACCAATTTTCAGCAACTGGCTTGCTACTACCTCAGCATATT 314  
Db 241 TAATGTCTCAGCAATACCAAGCAATTTCAAGATCTGG-GTGTTACTAGCCTCAGCATATT 299  
Qy 315 TTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTTATTTTCTTCCACTTAAAGAGGAGT 374  
Db 300 TCAATTTGCTCAGACTGCCAAATTTCTCCAACTTTTATTTTCTCCACTTAAAGAAAGGAT 359  
Qy 375 TAAGAGTGTCAATTCGTGTGATGTTGGTGGGCCCTTTGCTATTTTGGCTTTGTCATCTTTT 434  
Db 360 TAAGAATGTTGGTTTGGTGATGCTGTTGGGGCCCTTGCTATTTTTCATTTTGTAAATCTTGC 419  
Qy 435 TGTGATAAACAATGAGATGTTGGCGGACAAAAGAAATTTGAAGGAAACATGACTTGGAA 494  
Db 420 TCTGATAAACCACGGGTGAGAGTGTGGACAAAAGAAATATGAAGGAAATTTGTCTTGGAT 479  
Qy 495 GATCAAAATTCAGAGTGCATGTACTTTTCAAAATATGACTGTAAACCATGTTAGCAAACTT 554  
Db 480 GATCAAAATTCAGGAATGCATACAGCTTTCAAACTTGACTGTAAACCATGCCAGCAACGT 539  
Qy 555 AGTACCCCTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGTTTCTTTGTGTAACA 614  
Db 540 CACACCCCTGCACCTGACACTAATATCTTTTCTGCTGTTTATCTTCTCATGTAAACA 599  
Qy 615 TCTCAAGAAGATGAGCTCC 634  
Db 600 TGTCAAGAAGATGAGCTCC 619

## RESULT 9

US-09-925-065A-300418

; Sequence 300418, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 300418

; LENGTH: 619

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-300418

Query Match 44.6%; Score 415.2; DB 7; Length 619;

Best Local Similarity 81.5%; Pred. No. 2.3e-88;

Matches 505; Conservative 0; Mismatches 113; Indels 2; Gaps 2;

16 CCCATCATTTTTTCCAGTCTGGTAGTGTATACATTTGTTATGGAATTTTGTCTAATGGC 75

1 CTCATCATTTTATCAATTCGTGTAGTGTGTTGCAATTTGTTCTTGGAAATGTTGCCAATGGC 60

```
QY 76 TTCTAGCAGCTGGTAAATTCATTGAGTGGTTCAAGACACAAAGATCTCTTTGCTGAC 135
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TTCTAGCTCTAGTAGTGTCTTGGTGGTTAAGACACAAAGATCTCATCAGCTGAC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 136 CAAA-TTCTCACTGCTCTGGGGCTCCAGAGTTGGTTTGTCTCTGGGTATTATTATAA 194
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CAAATTTCTCACTGCTCTGGTGGTCCAGAGTTGGTTTACTCTGGGTCAATATTACA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACTGCTTA 254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TTGGTATGCAACTGTGTTTAATTTGGCTTCATATAGATTAGAAGTAAGAAATTTTGGTTC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 255 TAAATATCTGGCAGTGAATCAACCATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 TAATGTCTCAGCAATAACAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 TTATTGTCTCAAGATTGCAATTTCTCCAACCTTTATTTTCTTCACTTTAAAGAGAGAGT 374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 300 TCATTTGCTCAAGACTGCCAATTTCTCCAACCTTATTTTCTCCAACCTTAAAGAAAGGAT 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 TAAGAGTGCATCTGGTGTAGTGTGGGGCTTTGCTATTTTGGGCTTGTCTATCTTTT 434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 360 TAAGAATGTGGTTTGGTGTGCTGTGGGGCCCTTGGTATTTTTCATTTGTAATCTTGC 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 TGTGATAACATGAATGAGATTGTGCGGACAAAAGAAATTTGAAGGAAACATGACTTGGAA 494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 420 TCTGATAACACGGGTGAGAGTGTGGACAAAAGAAATATGAGGAAATTTGTCTTGGAT 479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 GATCAAAATTGAAGAGTGAATGTACTTTTCAAAATATGACTGTAACCATGGTAGCAAACTT 554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 480 GATCAAAATTGAGGAATGCAATACAGCTTTCAAACCTTGACTGTAACCATGCCAGCAACGT 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 AGTACCTTCACTCTGACCTACTATCTTTTATGCTGTATCTGTTTCTTTTGTGTAAACA 614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 540 CACACCTTGCATCTGACACTAATATCTTTTCTGCTGTATCTATTTCTCCATGTAAACA 599
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 TCTCAAGAAGATGCAGCTCC 634
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 600 TGTCAAGAAGATGCAGCTCC 619
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 10
US-09-925-065A-300417
; Sequence 300417, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300417
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-300417
```

Query Match 44.6%; Score 414.8; DB 7; Length 619;  
Best Local Similarity 81.3%; Pred. No. 2.8e-88;  
Matches 504; Conservative 1; Mismatches 113; Indels 2; Gaps 2;

```
QY 16 CCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTTGGAATTTTGTCTAATGCG 75
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 CTCATCATTTTATCAATTCCTGGTAGTGTTCGATTTTGTCTTTGGAATGTTGCCAATGCG 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 76 TTCTAGCAGCTGGTAAATTCATTGAGTGGTTCAAGACACAAAGATCTCTTTTCTGCTGAC 135
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TTCTAGCTCTAGTAGTGTCTTGGTGGTTAAGACACAAAGATCTCATCAGCTGAC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 136 CAAA-TTCTCACTGCTCTGGGGCTCCAGAGTTGGTTTGTCTCTGGGTATTATTATAA 194
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CAAATTTCTCACTGCTCTGGTGGTCCAGARTTGGTTTACTCTGGGTCAATATTATTACA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 195 CTGTGATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACTGCTTA 254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TTGGTATGCAACTGTGTTTAATTTGGCTTCACATAGATTAGAAGTAAGAAATTTTGGTTC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 255 TAAATATCTGGCAGTGAATCAACCATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 TAATGTCTCAGCAATAACAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 TTATTGTCTCAAGATTGCAATTTTCTCAAACCTTTATTTTCTTCACTTTAAAGAGAGAGT 374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 300 TCATTTGCTCAAGACTGCCAATTTCTCCAACCTTATTTTCTCCAACCTTAAAGAAAGGAT 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 TAAGAGTGCATCTGGTGTAGTGTGGGGCTTTGCTATTTTGGGCTTGTCTATCTTTT 434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 360 TAAGAATGTGGTTTGGTGTGCTGTGGGGCCCTTGGTATTTTTCATTTGTAATCTTGC 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 TGTGATAACATGAATGAGATTGTGCGGACAAAAGAAATTTGAAGGAAACATGACTTGGAA 494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 420 TCTGATAACACGGGTGAGAGTGTGGACAAAAGAAATATGAGGAAATTTGTCTTGGAT 479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 GATCAAAATTGAAGAGTGAATGTACTTTTCAAAATATGACTGTAACCATGGTAGCAAACTT 554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 480 GATCAAAATTGAGGAATGCAATACAGCTTTCAAACCTTGACTGTAACCATGCCAGCAACGT 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 AGTACCTTCACTCTGACCTACTATCTTTTATGCTGTATCTGTTTCTTTTGTGTAAACA 614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 540 CACACCTTGCATCTGACACTAATATCTTTTCTGCTGTATCTATTTCTCCATGTAAACA 599
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 TCTCAAGAAGATGCAGCTCC 634
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 600 TGTCAAGAAGATGCAGCTCC 619
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 11
US-10-301-480-250660/c
; Sequence 250660, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250660
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-250660
```

Query Match 44.2%; Score 411; DB 12; Length 525;  
Best Local Similarity 86.3%; Pred. No. 2.2e-87;  
Matches 453; Conservative 1; Mismatches 71; Indels 0; Gaps 0;



136	Qy	CAAAATTCACATGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTATTTATTTAAAC	195
525	Db	CAAAATTCACATGCTCTGGCGGTCTCCAGAAATGGTTGGTCTCTGGGCATTTATTTAAAT	466
136	Qy	TGGTATTCCAACTGTGTGNAATCCAGCTTTTATAGTGTAGAAGTAACTACTGCTTAT	255
465	Db	TGGTATTTAACTGTGTGNAATCCAGCTTTTATAGTGTAGAATTAAGAATTAATCTTCTTAT	406
256	Qy	AATATCTGGGGAGTGCATCAACCAATTTCCAGCAACTGGCTTGTCTACTACCCCTCAGCATATTT	315
405	Db	AATGCCTGGGTGTAAACCAACATTTCCAGCATGTGGCTTGTCTTAACCTCAGCATATTT	346
316	Qy	TATTTGCTCAAGATTGCCAATTTCTCCAACTTTTATTTTCTTCACTTAAAGAGGAGAGTT	375
345	Db	TATTTGCTCAAGATTGCCAATTTCTCCAACTTTCTTTTTCTTCATTTAAAGAGGAGAGTT	286
376	Qy	AAGAGTGCATCTCGTGATGTTGTTGGGGCCCTTTGCTATATTTTGGCTTGTGATCTTTTTT	435
285	Db	AGGAGTGTCAATCTCGTGATCTGTGTGGGGACTTTTGATATTTTGGTTTGTCACTCTCTTT	226
436	Qy	GTGATAAACATCAATGAGATCTGTGGGACAAAGAAATTTGAAGGAACATGACTCTGGAG	495
225	Db	GTGGCAAAACATGGATGAGATGTTGGGCAGAGAAATATGAAGGAACATGACTGGGAAG	166
496	Qy	ATCAAAATGAAGAGTGCATGTACTTTTCAAAATATGACCTGTAAACCATGGTAGCAAACTTA	555
165	Db	ATGAAATTTAGGAATACAGTACATCTTTTCATATTTTGACTGTAACTACCCTATGGAGCTTC	106
556	Qy	GTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAAATCTGTTCTTTGTGTAAACAT	615
105	Db	ATACCCCTTACTCTGTCCCTGATACTTTTCTGATGCTAAATCTGTTCTCTGCTGRTAAACAT	46
616	Qy	CTCAAGAAAGATGCAGCTCCATGGTAAAGATCTCAAGATCCGAGC	660
45	Db	CTCAAGAAAGATGCAGCTCCATGGAGAGGATCGCAAGATCTCAGC	1

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RESULT 12
US-10-301-480-864069/c
; Sequence 864069, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: Identification in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 864069
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-864069

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405 AATGCCTGGGTTGTAACCAACCAATTTTCAGCATGTGGCTTGCTGTAACTCAGCATATTT 346  
 316 TATTTGCTCAAGATTGCGCAATTTCTCCAACTTTATTTTCTTCTCACTTAAAGAGGAGAGTT 375  
 345 TATTTGCTCAAGATTGCGCAATTTCTCCAACTTTCTTTTCTTCTCATTTAAAGAGGAGAGTT 286  
 376 AAGAGTGTCAATCTTGGTGATGTTGTGGGGCTTTGCTATTTTGGCTTGTGCATCTTTT 435  
 285 AGGAGTGTCAATCTTGGTGATGTTGTGGGGACTTTGTGGGGACTTTGTATTTTGGTTGTCTCTT 226  
 436 GTGATTAACATGAATGAGATTGTGGGACAAAGAAATTTGAAGGAACAATGACTTGGAG 495  
 225 GTGGCAACATGGATGAGAGTATGTGGGACAGAAGATATGAAGGAACAATGACTGGGAG 166  
 496 ATCAAAATTGAAGAGTGCAAATGACTTTTCAAATATGACTGTAACCATGGTAGCAACATTA 555  
 165 ATGAATTTGAGGAATACAGTACATCTTTTCATATTTGACTGTAACTACCTATGGAGCTTC 106  
 556 GTACCTTCACTCTGACCTACTATCTTTTATGCTGTGTTAACTGTGTTCTTTGTGTAACAT 615  
 105 ATACCTTTTACTCTGTCCCTGATATCTTTTCTGATGCTAACTGTGTTCTGTGTTAAACAT 46  
 616 CTCGAAGAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCAGC 660  
 45 CTCGAAGAGATGCAGCTCCATGGAGAGGATCGCAAGATCTCAGC 1

RESULT 13  
 US-10-301-480-251369/c  
 ; Sequence 251369, Application US/10301480  
 ; Publication No. US20060057564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
 ; TITLE OF INVENTION: in the Human Genome  
 ; FILE REFERENCE: 108827.137  
 ; CURRENT APPLICATION NUMBER: US/10/301,480  
 ; CURRENT FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 10/215,598  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/311,695  
 ; PRIOR FILING DATE: 2001-08-10  
 ; NUMBER OF SEQ ID NOS: 1226818  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 251369  
 ; LENGTH: 612  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-301-480-251369

Query Match	42.9%	Score 398.6	DB 12	Length 612
Best Local Similarity	81.3%	Pred. No. 1.9e-84		
Matches 497	Conservative 1	Mismatches 110	Indels 3	Gaps 3
Qy	135	CCAAATTCACAGTCTCGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTATTATTATAA	194	
Db	610	CAAAATTCACAGTCTCGTGGTGTCCAGAAATGGTTTACTCTGGGTCAATATTATTACA	551	
Qy	195	CTGGTATTCAACTGTGTGTAATCCAGCTTTTAAATAGTGTAGAAGTAAAGAACTACTGCTTA	254	
Db	550	TTGGTATCAACTGTGTTTAAATTTGGCTTCATATAGATTAGAAGTAAAGAAATTTTGGTTC	491	
Qy	255	TAATATCTGGCGAGTGNATCAACATTTTCAGCAACTGGCTTGCTACTACCTCAGCATATT	314	
Db	490	TAATGTCTCAGCAATAACCAAGCATTTTCAGCATTTGG-GTGTACTAGCCTCAGCATATT	432	
Qy	315	TTATTTGCTCAAGATTGCCAATTTCTCCAACCTTTATTTTCTTCACATTAAGAGGAGAT	374	
Db	431	TCATTTGCTCAAGCTGCCAATTTCTCCAACCTTATTTTCTCCAACCTTAAGGAAGGAT	372	
Qy	375	TAAGAGTGTCAATCTCGTGTATGTTGTGGGGCCCTTTGCTATATTTTGGCTTGTCACTCTTT	434	

Db 371 TAAAGATGTTGGTTGGTGATGCTGTGGGGCCCTGGGTATTTTTCATTTGTAATCTTGC 312  
Qy 435 TCTGATAACATGAATGAGATTGTGGGACAAAGAAATTTGAAGAAACATGACTTGGAA 494  
Db 311 TCTGATAACACCGGTGAGAGTGTGGGACAAAGAAATATGAAGAAATTTGCTTGGAT 252  
Qy 495 GATCAAAATTGAAGAGTGAATGACTTTTCAAAATATGACTGTAAACATGCTAGCAAACTT 554  
Db 251 GATCAAAATTGAGGAATGCATACAGCTTTCAAACTTGACTGTAAACATGCCAGCAACGT 192  
Qy 555 AGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTTAAATCTGTTCTTTGTAACA 614  
Db 191 CACACCCCTGCACTCTGACACTAATATCTTTCTGCTGGTAAATCTATTTCTCCATGTAACA 132  
Qy 615 TCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCAGCAACAAGGT-CCACA 673  
Db 131 TGTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCTCAGCAACAAGGTGCAACA 72  
Qy 674 TAAAGCTTTGCAAACTGTGATCT-CCCTCCCTCTGTTATGTCGCAATTTACTTTCTGTCC 732  
Db 71 TAAAGCTTTGCAAACTGGGATCTCCCTCCGTAATGTTATTTGCCATTTACTTTCTGTGT 12  
Qy 733 ATAATGATATC 743  
Db 11 ATAATCACATC 1

## RESULT 14

US-10-301-480-864778/c  
; Sequence 864778, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 864778  
; LENGTH: 612  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-864778

Query Match 42.9%; Score 398.6; DB 12; Length 612;  
Best Local Similarity 81.3%; Pred. No. 1.9e-84;  
Matches 497; Conservative 1; Mismatches 110; Indels 3; Gaps 3;  
Qy 135 CCAAAATTCCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTTATTATAA 194  
Db 610 CAAATTTCTCACTGCTCTGGGTGTCAGAAATGGTTTACTCTGGTCATATTATACA 551  
Qy 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAACTACTGCTTA 254  
Db 550 TTGGTATGCACTGTGTTTAAATTTGGCTTCATATAGATTAGAAGTAAGAATTTTGGTTC 491  
Qy 255 TAAATCTGGGAGTGATCAACCATTTCCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314  
Db 490 TAAATGCTCAGCAATTAACCAAGCATTTTCAGCATGTGG-GTGTACTAGCTCAGCATATT 432  
Qy 315 TTATTTGCTCAAGATGCGCAATTTCTCCAACTTTTATTTTCTTCACTTTAAAGAGGAGT 374  
Db 431 TCATTTGCTCAAGACTGCCAATTTCTCCAACTTATTTTCTCCACCTAAAGAGGAT 372  
Qy 375 TAAAGATGTCATCTGCTGATGTTGTTGGGCCCTTTGCTATTTTGGCTTGTGTCATCTTT 434  
Db 371 TAAAGATGTTGGTTGGTGATGCTGTGGGGCCCTGGGTATTTTTCATTTGTAATCTTGC 312

Qy 435 TCTGATAACATGAATGAGATTGTGGGACAAAGAAATTTGAAGAAACATGACTTGGAA 494  
Db 311 TCTGATAACACCGGTGAGAGTGTGGGACAAAGAAATATGAAGAAATTTGCTTGGAT 252  
Qy 495 GATCAAAATTGAAGAGTGAATGACTTTTCAAAATATGACTGTAAACATGCTAGCAAACTT 554  
Db 251 GATCAAAATTGAGGAATGCATACAGCTTTCAAACTTGACTGTAAACATGCCAGCAACGT 192  
Qy 555 AGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTTAAATCTGTTCTTTGTAACA 614  
Db 191 CACACCCCTGCACTCTGACACTAATATCTTTCTGCTGGTAAATCTATTTCTCCATGTAACA 132  
Qy 615 TCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCAGCAACAAGGT-CCACA 673  
Db 131 TGTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCTCAGCAACAAGGTGCAACA 72  
Qy 674 TAAAGCTTTGCAAACTGTGATCT-CCCTCCCTCTGTTATGTCGCAATTTACTTTCTGTCC 732  
Db 71 TAAAGCTTTGCAAACTGGGATCTCCCTCCGTAATGTTATTTGCCATTTACTTTCTGTGT 12  
Qy 733 ATAATGATATC 743  
Db 11 ATAATCACATC 1

## RESULT 15

US-10-301-480-251370/c  
; Sequence 251370, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 251370  
; LENGTH: 612  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-251370

Query Match 42.7%; Score 397.4; DB 12; Length 612;  
Best Local Similarity 81.3%; Pred. No. 3.7e-84;  
Matches 497; Conservative 0; Mismatches 111; Indels 3; Gaps 3;  
Qy 135 CCAAAATTCCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTTATTATAA 194  
Db 610 CAAATTTCTCACTGCTCTGGGTGTCAGAAATGGTTTACTCTGGTCATATTATACA 551  
Qy 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAACTACTGCTTA 254  
Db 550 TTGGTATGCACTGTGTTTAAATTTGGCTTCATATAGATTAGAAGTAAGAATTTTGGTTC 491  
Qy 255 TAAATCTGGGAGTGATCAACCATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314  
Db 490 TAAATGCTCAGCAATTAACCAAGCATTTTCAGCATGTGG-GTGTACTAGCTCAGCATATT 432  
Qy 315 TTATTTGCTCAAGATGCGCAATTTCTCCAACTTTTATTTTCTTCACTTTAAAGAGGAGT 374  
Db 431 TCATTTGCTCAAGACTGCCAATTTCTCCAACTTATTTTCTCCACCTAAAGAGGAT 372  
Qy 375 TAAAGATGTCATCTGCTGATGTTGTTGGGCCCTTTGCTATTTTGGCTTGTGTCATCTTT 434  
Db 371 TAAAGATGTTGGTTGGTGATGCTGTGGGGCCCTGGGTATTTTTCATTTGTAATCTTGC 312

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Qy 435 TGTGATAAATGATGAGATTGTGCGGACAAAGAAATTTGAAGGAAACATGACTTGGAA 494
Db ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
311 TCTGATAACCGGGTGAGAGTGTGTGCACAAAAGAAATATGAAGGAAATTTGTCTTGGAT 252
Qy 495 GATCAAAATTGAAGAGTGCATCTTTTCAAATATGACTGTAAACCATGGTAGCAAACTT 554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 GATCAAAATTGAGGAATGCAATACAGCTTTCAAACCTTGACTGTAAACCATGCCAGCAAAAGT 192
Qy 555 AGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGTTCTTTTGTGTAACA 614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191 CACACCCCTGCACTCTGACACTAATATCTTTCTGCTGGTAAATCTATCTCCATGTAAACA 132
Qy 615 TCTCAAGAGATGCAAGCTCCATGGTAAGGATCTCAAGATCCAGACCAAGGT-CCACA 673
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131 TGTCAAGAGATGCAAGCTCCATGGCAAGGATCTCAACATCTCAGCACCAAGGTGCAACA 72
Qy 674 TAAAGCTTTGCAAACTGTGATCT-CTTCCTCTTGTATGTGCCATTTACTTTCTGTCC 732
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
71 TAAAGCTTTGCAAACTGGGATCTCCCTTCGGTATGTTATTTGCCATTTACTTTCTGTGT 12
Qy 733 ATAATGATATC 743
Db ||||| |||||
11 ATAATCACATC 1
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